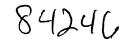
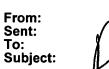
STIC-Biotech/ChemLib





Chan, Christina

Tuesday, January 14, 2003 3:06 PM Holleran, Anne; STIC-Biotech/ChemLib RE: RUSH sequence search for 09/506,079

Imp rtance:

西松。梅

High

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message----

From: Holleran, Anne

Tuesday, January 14, 2003 12:12 PM Sent: Chan, Christina

To:

Subject:

RUSH sequence search for 09/506,079

Please approve and forward to STIC the following RUSH sequence search request. This is for an amendment due this biweek. Thanks.

Please search the following for 09/506,079:

commercial and interference databases oligomer search of SEQ ID NO: 1(aa)

commercial and interference databases oligomer search of SEQ ID NO: 2(aa)

SEQ ID NO: 1 is a fragment of SEQ ID NO: 2.



Point of Contact: Barb O'Bryen **Technical Information Specialist** STIC CM1 6A05 308-4291

1 20	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher: <u>Molb</u>	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up:/	Bibliographic:	DRLink:
Date Completed: 1-15-03	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

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8

protein

Sequence

37, Appl 37, Appl 37, Appl 37, Appl 81, Appl 81, Appl 15, Appl 15, Appl 273, Appl 27, Appli 4, Appli 4, Appli 4, Appli 4, Appli 4, Appli 14, Appli 15, Appli 16, Appli 17, Appli 18, Appli 19, Appli 19, Appli 19, Appli 10, Appli 11, Appli 11, Appli 11, Appli 11, Appli

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Post-processing: Listing first 45 summaries
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US-08-469-560-49
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US-09-630-155-1
                                                                                                Query Match
Best Local S
Matches 17
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Patent No. 6414130
GENERAL INFORMATION:
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 206 628-7621
TELEPHONE: 206 628-7629
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 79
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                                                                 37
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COMPUTER: PC compatible
OPERATING SESTEM: Windows95
SOFTWARE: WORD
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/630,155
FILING DATE: 16-Jan-2001
                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: HER-2 ECD antagonist
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Doherty, Joni Kristin and Gail M. (TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
                                  VSAFYSLPLAPLSPTSV
                                                   VSAFYSLPLAPLSPTSV 53
                                                                                                  l Similarity
17; Conserv
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STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                NAME: Davison, Barry L. REGISTRATION NUMBER: 47,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DAVIS WRIGHT TREMAINE LLP STREET: 1501 Fourth Avenue, 2600 Century Square
                                                                                                  Conservative
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PCT-US95-06846A-37

US-08-118-270-81

PCT-US95-08528-81

US-09-134-001C-4092

US-08-565-386-15

US-09-615-192A-273

US-09-386-653A-7

US-09-386-653A-7

US-09-088-651-2

US-09-088-651-2

US-09-088-651-2

US-09-108-653A-7

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Pred. No.
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DB 4; . 5e-10;

Length 79

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Gaps

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No.

Minimum Maximum

DB

Total number Word size Scoring table: Sequence: Title: Perfect score:

Searched:

Database :

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STRANDEDNESS: STRAIGLE
TOPOLOGY: unknown
MOLECULE TYPE: polypeptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-630-155-2
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US-09-630-155-2
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Matches 17;
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Patent No. 6414130
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Sequence 11,
Patent No. 5
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                                                                                                                                                                                                                                                                                              GENERAL
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TELEFAX: 206 628-7699
INFORMATION FOR SEQ ID NO: 2:
                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                            TITLE OF INVENTION: SECRETED TITLE OF INVENTION: ENCODING
                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                              APPLICANT:
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                                STATE:
                                                            STREET:
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                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/630,155
FILING DATE: 16-Jan-2001
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
OPERATING SYSTEM: Windows95
SOFTWARE: WOrd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Doherty, Joni Kristin and Gail M. Clinton TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                           INFORMATION:
02140
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                                             Cambridge
                              ΜA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Davison, Barry L. REGISTRATION NUMBER: 47,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Washington COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                         Application US/09014969
                                                            E: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                     Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
               U.S.A.
                                                                                                                                                                                                                                           McCoy, John M.
LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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1501 Fourth Avenue, 2600 Century Square
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 15:
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
                 PRIOR APPLICATION DATA:
                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC\_DOS/MS\_DOS
SOFTWARE: PatentIn Release #1.0, \
APPLICATION NUMBER:
                                  CLASSIFICATION:
                                             APPLICATION NUMBER: US 08/580,555 FILING DATE: 29-DEC-1995
                                                                                              CLASSIFICATION: 435
                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                STREET:
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CHONG, SHAORONG S.C.
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PROTEINS, METHODS OF THEIR

PRODUCTION AND METHODS FOR PURIFICATION OF TARGET

PROTEINS
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US 08/496,247
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Pred. No.
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                                                                                                                                                         Version #1.25
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FILING DATE: 2: CLASSIFICATION:

28-JUN-1995

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US-08-036-555B-49
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Best Local S
Matches 6
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555B
FILING DATE: 24-MAR-1993
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Glial Mitogenic Fac
TITLE OF INVENTION: Preparation and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 508-927-5054
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                 COMPUTER:
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APPLICATION NUMBER: 07/907,138 FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
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                                                                                                                                                                                                                                                             Diskette, 5.25 inch, 360 kb storage
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100.0%; Pred. N
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RESULT 6
US-08-469-569-49
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Matches
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INFORMATION FOR SEQ
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/90
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                             PRIOR APPLICATION DATA:
                                                                          PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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APPLICANT: Minghetti,
APPLICANT: Chen, Maio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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PULICATION NUMBER: 08/0
PULICATION NUMBER: 08/0
PULICATION NUMBER: 08/0
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les 6; Conservative
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                                          APPLICATION NUMBER: 07/863,703 FILING DATE: 03-APRIL-1992
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                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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              APPLICATION NUMBER:
                                                                                                                                      FILING DATE:
                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                          FILING DATE:
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Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
Chen, Maio Su; Hiles, Ian
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                                                                                                                                                                                23-OCT-1992
                                                                                                                                    03-SEP-1992
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03-APRIL-1992
MBER: U.K. 91 07566.3
10-APRIL-1991
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100.0%; Pred. N
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                                                                                                                                                                                                                                                                                                                                                              360 kb storage
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RESULT 7
US-08-249-322A-49
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Best Local (
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APPLICANT:
                                            ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: LUI
TELECOMMUNICATION INFORMATION:
                                                                                         PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: 07/940,389
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Glial Mitogenic Factoriate of INVENTION: Preparation and Use
                                                                                                     APPLICATION NUMBER: 07/863, FILING DATE: 03-APRIL-1992
                                                                             APPLICATION NUMBER:
                                                                                                                                                     APPLICATION NUMBER: 07/90 FILING DATE: 30-JUN-1992
                                                                                                                                                                                                     FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/96 FILING DATE: 23-0CT-1992
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/036,555 FILING DATE: 24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/249,322A FILING DATE: 26-MAY-1994
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minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
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           Christine H.
NUMBER: 34,266
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                                                        UMBER: U.K. 91 07566.3
10-APRIL-1991
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N: Glial Mitogenic I
NUMBER:
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LUD 250.4
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Pred. No
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Patent No.
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Query Match
Best Local Similarity
""tches 6; Conserve
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TELEFAX: 617-42
INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                            TELECOMMUNICATION INFORMATION:
                                                                                                       FILING DATE: 10-APR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/96
APPLICATION NUMBER: 07/96
APPLICATION NUMBER: 07/96
APPLICATION NUMBER: 07/96
                              TELEPHONE:
                                                            REFERENCE/DOCKET NUMBER:
                                                                         NAME: Bieker-Brady, Kristina REGISTRATION NUMBER: 39,109
                                                                                                                                     APPLICATION NUMBER: U.K.
                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                                                                                                                                                                  APPLICATION NUMBER:
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176 Federal Street
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                 617-428-7045
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Minghetti, Luisa
Waterfield, Michael
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Chen, Maio Su
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                                                                                                                                                   03-APRIL-1992
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                                                            04585/00200A
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Pred. No.
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RESULT 9
US-08-734-591A-49
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Best Local Similarity luv.
""+"ches 6; Conservative
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                                                                                                                                                                                              FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
PRIOR TOWNSON NUMBER: 07/907,138
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
                                                                                                                                                  PRIOR APPLICATION NUMBER: 07/90/,150
ETLING DATE: 30-UN-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
07/863,703
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-OCT-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                             ATTORNEY/AGENT INFORMATION:
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                                 NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200P
                                                                                               APPLICATION NUMBER: UK 91 07566.3 FILING DATE: 10-APR-1991
                                                                                                                                        APPLICATION NUMBER: 07/80 FILING DATE: 03-APR-1992
                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/94 FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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Stroobant, Paul
Minghetti, Luisa
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tive 0; Misma
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Query Match
Best Local Similarity
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                                                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,660
FILING DATE:
                                                                                                                                                                                 NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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ADDRESSEE: Fish & Richardson
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                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/9: FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 01-DEC
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/01
FTI.ING DATE: 29-JAN-1993
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ZIP: 0211-2804
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                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS
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                                                                                                        LENGTH:
                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                   (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                               10-AUG-1992
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 7.6%;
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Pred. No. 10;
 Score 6; DB 2;
Pred. No. 10;
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                 Length 15;
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; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-470-335-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bos taurus
US-08-341-018-82
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Best Local Similarity 100.0%; P
Matches 6; Conservative 0;
                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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LENGTH: 15
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APPLICANT: McBurney, Robert N.
TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF
TITLE OF INVENTION: CELLULAR COMMUNICATION
FILE REFERENCE: 04585/041001
CURRENT APPLICATION NUMBER: US/08/341,018A
CURRENT FILING DATE: 1994-11-17
NUMBER OF SEQ ID NOS: 87
NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE FILE REFERENCE: 04585/00200B
CURRENT APPLICATION NUMBER: US/08/470,335F
CURRENT FILLING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STROOBANT, PAUL
APPLICANT: MATERFIELD, MICHAEL
APPLICANT: MATERFIELD, MICHAEL
APPLICANT: MARCHIONNI, MARK
                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1993-03-24
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        56 SPVSVG 61
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| SPVSVG 7
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Marchionni, Mark A.
Bermingham-McDonogh, Olivia
Goldin, Stanley M.
                                                         Conservative
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100.0%; Pr
                                                       7.6%; Score 6; DB / 100.0%; Pred. No. 10; lve 0; Mismatches
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US-08-735-021-49
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 49
LENGTH: 15
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Patent No.
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                     APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC
TITLE OF INVENTION: PREPARATION AND
NUMBER OF SEQUENCES: 187
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                                       COUNTRY: UZIP: 02110
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                                                                       Massachusetts
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                                                       U.S.A.
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Waterfield, Michael
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1992-04-03
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CURRENT APPLICATION DATA:

COMPUTER: IBM Compatible Pentium OPERATING SYSTEM: Windows95

FastSeq Version 2.0

US/08/734,664A

APPLICATION NUMBER: US/08 FILING DATE: 22-OCT-1996 CLASSIFICATION: 536

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GENERAL INFOMATION:
GENERAL INFOMATION:
APPLICANT: GOODEARL, ANDREW
APPLICANT: STROOBANT, PAUL
APPLICANT: MATERFIELD, MICHAEL
APPLICANT: MARCHTONI, MARK
APPLICANT: MARCHTONI, MARK
APPLICANT: HILES, IAN
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
CURRENT APPLICATION NUMBER: US/08/470,339C
CURRENT FILLING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
EARLIER APPLICATION NUMBER: 07/940,389
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US-08-470-339-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bleker-Brady, Kristina REGISTRATION NUMBER: 39,109 REFERENCE/DOCKET NUMBER: 04585/00200J TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 428-0200 TELEFAX: (617) 428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UK 9: FILING DATE: 10-APR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/96 FILING DATE: 23-OCT-1992 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/2:
FILING DATE: 26-MAY-1994
PRIOR APPLICATION DATA:
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10-APR-1991
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; TYPE: PRT; ORGANISM: Bos taurus US-08-470-339-49
Search completed: January 14, 2003, 17:15:45 Job time: 6.0763 secs
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SEQ ID NO 49
LENGTH: 15
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Best Local Similarity
Matches 6; Conserv
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EARLIER APPLICATION NUMBER: 07/907,138
EARLIER FILING DATE: 1992-06-30
EARLIER APPLICATION NUMBER: 07/863,703
EARLIER FILING DATE: 1992-04-03
EARLIER APPLICATION NUMBER: 91 07566.3 GB
EARLIER FILING DATE: 1999-04-10
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                                                                                           56 SPVSVG 61
                                                                          2 SPVSVG 7
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Q9ERV6
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Q9QX70
Q9EP98
Q63365
Q9QZ16
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                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parameters:
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018735 canis famil
                                                                                                                                                                                              Description
                                                                                                                                                                      Q9uk79 homo sapien
Q90836
Q9psh2
Q9psh2
Q9wvf5
Q9wvf5
Q9qx70
Q9ep98
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Q9i314 pseudomonas	.6 Q9I314		1.7	45 7	•
	P95438		1.7	4 7	•
Q9jn88 streptomyce			1.7		•
Q9i3n6 pseudomonas	16 Q913N6		1.7	42 7	۰,
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Q9z3z2 pseudomonas	o		1.7	0 7	
Q96cm4 homo sapien			1.7	9	w
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			1.7	7 7	w
			1.7	6 7	w
Q9fmc7 arabidopsis	.0 Q9FMC7		1.7	5 7	w
∙	Q9XPE3		1.7	4 7	w
Q8ueq6 agrobacteri	.6 Q8UEQ6		1.7	3 7	w
Q9nmrl leishmania	Q9NMR1		1.7	32 7	w
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Q9wtz9 mus musculu			1.7	27 7	N
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                                                                                                                                   Query Match
Best Local S
Matches 83
                                                                                                                                                                                                                                                                                              Doherty J.K., Clinton G.M., Adelman J
Submitted (SEP-2000) to the EMBL/GenE
EMBL; AF177761; AAD56009.2;
InterPro; IPR000494; EGFR_L_domain.
InterPro; IPR002174; Furin-like.
Pfam; PF01030; Recept_Ldomain; 1.
Pfam; PF01030; Recept_Ldomain; 1.
SMART; SM00261; FU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UK79 PRELIMINARY;
Q9UK79;
01-MAY-2000 (TIEMBLIFEL 13, C
01-MAR-2001 (TIEMBLIFEL 16, L
01-JUN-2002 (TIEMBLIFEL 21, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99415951; PubMed=10485918;
MEDLINE=99415951; PubMed=10485918;
Doherty J. K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
"The HER-2/neu receptor tyrosine kinase gene encodes a secret autoinhibitor.";
autoinhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999).
NCBI_TaxID=9606;
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                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                      419 AA;
                                                                                                                                      Conservative
                                                                                                                     19.8%; 5cc
100.0%; Pr
                                                                                                                                                                                                                                                                  45472 MW; FEC1BE347E2D030C CRC64;
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Last annotation update)
                                                                                                                                   Score 83; DB; Pred. No. 5.6
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Matches 51
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01-JAN-1998
01-JUN-2002
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                  "cDNA cloning of erbB-2 from canine mammary gland."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases EMBL; AB008451; EMAZ31127.1; -. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klonisch T., Wolf P.,
Tetens F., Fischer B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Klonisch T., Wolf P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence of control (TrEMBLrel. 18, Last annotation)
Receptor tyrosine kinase ErbB2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BG66
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis
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                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
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                                                                                                                                                                                             [nterPro;
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PF02757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            familiaris (Dog).
yota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.
51; Conservative
                                                                                                            ; IPR000494; EGFR_L_domain.
; IPR000719; Euk_pkinase.
; IPR002174; Furin-1ike.
; IPR001245; Tyr_pkinase.
; IPR004019; Yrp_motif.
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                             YLP;
                                                                                             Furin-like; 1.
                                                                            pkinase;
                                                 Recep_L_domain;
    Euk_pkinase;
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Euk_pkinase.
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; Fissipedia; Canidae;
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annotation update)
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2.7e-44;
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01-NOV-1996 (TrEMBLrel. 01
01-NOV-1996 (TrEMBLrel. 0:
01-JUN-2002 (TrEMBLrel. 2
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Best Local
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SMART; SM002b1; TYRC; 1.
PROSITE; PS0001B; EF_HAND; UNKNOWN_1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46
SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46
SEQUENCE FROM N.A. MEDLINE=92123214; Telickinger T.W., M
                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                              Gallus gallus (Chicken).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of a novel EGFR-related peptide: A puregulator of EGFR.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AF187818; AAG17037.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                  Q90836
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TISSUE-GASTRO-DUODENAL MUCOUS;
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                                                       NCBI_TaxID=9031;
                                                                      Gallus
                                                                                   Archosauria;
                                                                                                                               C-ERBB.
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InterPro; IPR002174; Furin-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Furin-like;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor
              PubMed=1732751;
                                                                                     Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                   53233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%;
100.0%;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Majumdar
                                                                                                                                        . 01, Created)
. 01, Last sequence update)
. 21, Last annotation update)
precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16, Created)18, Last sequence update)21, Last annotation update)receptor related protein.
                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                         Score 9;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50;
Pred. No.
                                                                                                Craniata;
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   CF873A8376C519E5 CRC64;
                                                                                     Galliformes;
                                                                                                                                                                                                                                                                                                                                            Mismatches
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2;
                                                                                                Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..9e-42;
s 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A putative negative
                                                                                   Phasianidae;
                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1259;
                                                                                                                                                                                                                                                                                                                                                                      Length 478;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281
                                                                                   Phasianinae;
                                                                                                                                                                                                                                                                                                                                            0
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Kung

H. -J.;

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RESULT
Q9ERV6
ID Q9
AC Q
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1 Ol-JUN-2002 (TrEMBLrel. 21, Last sequence update)

2 Epidermal growth factor receptor (Fragment).

3 Gallus gallus (Chicken).

3 Eukaryota; Metazoa; Chordata; Cram''-

Archosauria; Aves; Neognar'

Gallus.

NCRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                      Q9ERV6;
Q9ERV6;
01-MAR-2001
01-MAR-2001
                                                                                         EGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dependent transformation.";
Mol. Cell. Biol. 12:883-893(1992).
EMBL; M77637; AAA48759.1;
InterPro; IPRO00494; EGFR_L_domain.
InterPro; IPRO02174; Furin-like.
                                                                                                                                        01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              implication in oncogenic activation
Oncogene 8:2939-2948(1993).
InterPro; IPRO00494; EGFR_L_domain
InterPro; IPRO02174; Furin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kung
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Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 2.
                                                           Mus
                                                                                                             Epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00757; Furin-like; 2. Pfam; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Callaghan T., Antczak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=94020816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "An alternatively soluble, truncated
                                                                                                                                                                                                                                                                                                                                                                                                          393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 QCAAGCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete description of the EGF-receptor exon structure:
musculus (Mouse)
aryota; Metazoa; (
malia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCAAGCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      н. J.
                                                                                                                                                                                                                                                                                                                                                                                                          QCAAGCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCAAGCTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         599 AA;
                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          4:01
                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
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                                                                                                                   factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-8414496;
czak M., Flickinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    processed
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527
58353
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Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66363 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%;
                                                                                                             16, Created)16, Last sequence update)21, Last annotation updatreceptor isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d mRNA from the avian c-erbB gene encodes
the receptor that can block ligand-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
EGF/TGF-ALPHA RECEPTOR.
764564ABCC095298 CRC64;
Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEAB46D293D991BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
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                                                                                                                                                                                                                                                               643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . DB
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                                                                                                                                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers M.
  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9WVP5;
Q9WVP5;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
7-1/armal growth factor receptor (Epidermal growt
                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
129/SVJ, AND 129/SVEVTAC;
STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen / Reiter J.L., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00757; F
Pfam; PF01030; R
SMART; SM00261;
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=LIVER;
MEDLINE=21085660; PubMed=11217
                                                                                                                                                                                                                                                                                                                             "Alternative Transcripts from the Human and Carboxy-Terminal Truncated Receptors."; Submitted (JAN-1999) to the EMBL/GenBank/DDE
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-LIVER;
Reiter J.L., Threadgill D.W., I
Lampland A.L., Balasubramaniam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2000) to the EMBL; AF275366; AAG28046.1; EMBL; AF275364; AAG28046.1; EMBL; AF275365; AAG28046.1; MGD; MGI:95294; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C3H/101, 129/SVJ, AND 129/SVETTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland C.D., Lampland B.L., Crossley T.O., Magnuson T.R., James C.D., Malasuka
                                                                                                                               mouse alternative
                                                                                                                                                                                                                                                                                                                                                                                                 Lampland A.L., Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9WVF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                        Submitted
                                                                                                                               "Comparative genomic sequence analysis mouse alternative Egfr transcripts enco
                                                                                                                                                                             Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maihle N.J.;
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                                                                                      (JUN-2000)
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n S., Crossley
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shbata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local s
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Pfam; PF00757;
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Arakawa T.,
   Submitted [3]
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90258888; PubMed=2342466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                               Petch
                                                                                                              STRAIN-FISHER;
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                                                                                                                                                      SEQUENCE FROM N.A.
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9; Conser
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IPR002174;
                                       (NOV-1991)
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                                                                                                                  TISSUE-LIVER;
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Furin-like; 1.
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                                   EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                V.W., Blasband A.J., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6B34063B1BC928CB CRC64;
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Query Match
Best Local
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InterPro; IPR000494; EGFR_L_c
InterPro; IPR000719; Euk_pkii
InterPro; IPR002174; Furin-1:
InterPro; IPR0021245; Tyr_pkii
Pfam; PF00757; Furin-1ike; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0109; TYRKINASE.

ProDom; PD000001; EUK_PKINASE; 1.

SMART; SM00261; FU; 3.

SMART; SM00219; TYFKC; 1.

PROSITE; PS001107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
HSSP;
                                                                                              mouse alternative Egfr transcripts enco
                                                                                                                                                                                                                                                                                                                        STRAIN-C3H/101, 129/SVJ, AND 129/SVEYTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.
Sinclair C.S., Pearsall R.S., Green P.J., Yee D.,
Balasubramaniam S., Crossley T.O., Magnuson T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Epidermal growth factor
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STRAIN=FISHER: TISSUE=LIVER;
Guttridge K., Dawson T.L., E
Submitted (NOV-1999) to the
                                                                                                                                                           Reiter J.L., Threadgill D.W., Eley G.D., Schehl C., Pearsall R.S., Green P.J., Yee Balasubramaniam S., Crossley T.O., Magnuso
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C3H/101, 129/SVJ,
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Receptor; SEQUENCE 1209 AA; 1:
                                                                                                                                                                                                     STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                mouse alternative
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                                                                                                                                                  Maihle N.J.;
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                                                                                                                                                                                                                                                                  isoforms
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P11362; 1FGK.
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nilarity 100.0%;
Conservative 0
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Recep_L_domain;
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TISSUE=LIVER;
-- T.L., Earp H.S.
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                                                                                                                                                                                                                                                                             mic sequence analysis and isolation of human and Egfr transcripts encoding truncated receptor
                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r; Transferase; Tyrosine-protein kinase. 134891 MW; 96FEE7F6CC1B7773 CRC64;
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16, Last sequence update)
21, Last annotation updat
receptor isoform 1.
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Pred. No
                                                                                      EMBL/GenBank/DDBJ
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ee D., Lampland .
uson T.R., James
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RESULT 12
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Best Local
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                                                                                                                        Oncogene;
NON_TER
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Q63365;
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SMART; SM00220; S_TKC; 1.

SMART; SM00210; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00110; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 0), Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00757; Furin-like; 1. Pfam; PF00069; pkinase; 1. Pfam; PF01030; Recep_L_domain;
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91061737; PubMed=2123292;
Suen T.C., Hung M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Rec
                                                                                                                                          EMBL; M61004; AAA41686.1;
                                                                                                                                                    Mo1
                                                                                                                                                                             Yan D.H., Hung M.C.;
                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-91172172; PubMed-1672439;
                                                                                                                                                                                                                             Suen T.C., Hung M.C.; "Multiple_cis- and trans-acting elements involved
                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                   Transforming oncogene NEU (Fragment).
Rattus norvegicus (Rat).
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InterPro; IPR001245;
                                                                                                                                                                   "Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                    239
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                                                                                       Local
                                                                                               Match
                                                             LLALLPPG 19
                                                                                                                                                                                                                                                                                                                                                                                                                    QCAAGCTGP
                                                                                                                                                  Cell. Biol. 11:1875-1882(1991)
                                                                                                                                                                                                                                                                                                                                                                                                  QCAAGCTGP
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                                            LLALLPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
9; Conserv
                                                                              Similarity
8; Conserv
                                                                                                                         Transforming protein.
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                                                                                                                 48 AA;
                                                                             1.9%; S larity 100.0%; Conservative 0;
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
 PRELIMINARY;
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210 AA; 134840
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                                                                                                                4966 MW;
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Tyr_pkinase.
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EGFR_L_domain.
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34840 MW; 62CD021C9DE32E18
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Pred. No.
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Sciurognathi;
 PRT;
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                                                                                                                                                                   of.
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thi; Muridae;
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; Murinae; Rat
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RESULT 14
008558
ID 00855
AC 00855
DT 01-U
DT 01-U
DT 01-U
DT 10400
CS Rattu
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Q9QZI5
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Best Local S
Matches 8
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Best Local 9
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NON_TER
SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAY-2000 (TrEMBLrel. 13, Last annotation
01-MAY-2000 (TrEMBLrel. 13, Last annotation
Carbonyl reductase isoform I (Fragment).
                      01-JUL-1997 (TrEMBLrel. 04, C
01-JUL-1997 (TrEMBLrel. 04, L
01-DEC-2001 (TrEMBLrel. 19, L
Inducible carbonyl reductase.
                                                                                                                                                                                                                                                                                          STRAIN-WISTAR; TISSUE-OVARY;
Espey L.L., Yoshioka S., Russell D., Ujioka T.
Fujii S., Okamura H., Richards J.S.;
"Characterization of Ovarian Carbonyl Reductas
Ovulation in the Gonadotropin-Primed Immature
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QZI5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AI
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"Characterization of Ovarian Carbonyl Reductase Ovulation in the Gonadotropin-Primed Immature Ra Submitted (AUG-1999) to the EMBL/GenBank/DDBJ da EMBL; AF181955; AAF03394.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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              Rattus norvegicus
                                                                           008558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carbonyl reductase isoform II (Fragment).
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Similarity 100.0%;
8; Conservative
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8; Conser
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 Metazoa;
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 Craniata; Vertebrata;
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RESULT 15
Q924V3
Search completed: January 14, Job time: 49.2751 secs
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Q924V3;
Q1-DEC-2001 (
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Q1-MAR-2002 (
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Terada T., Sugihara Y., Nakamura K.;

Terada T., Sugihara Y., Nakamura K.;

"Chinese hanster carbonyl reductase.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

(SDR) FAMILY.

(SDR) FAMILY.

EMBL; AB043541; BAB62840.1; -.
                                                                                                                                                                                      InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
Oxidoreductase.
SEQUENCE 277 AA; 30498 MW; 2F7E876E
                                                                                                                                                                                                                                                                                                                                                                                                                                Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase.
SEQUENCE 277 AA; 30654 MW; DDA015D1B71673A7 CRC64;
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Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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STRAIN-WISTER; TISSUE-OVARY;
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nes 8; Conserv
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nes 8; Conserv
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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100.0%; Pr
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                2003, 17:14:25
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Minimum DB seq length: 0
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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568.337 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result

esult No.	Query Score Match	Query Match Length DB	BG	ID	Description
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9	19		9	US-09-854-356-7	, D
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12	19		9	US-09-854-356-1	Sequence 1, Appli
13	19		9	US-09-930-125-2	2
14	19		10	US-09-811-123-9	9
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US-09-764-864-896	US-09-771-161A-149	US-09-925-301-988	US-09-925-300-1678	US-09-981-876-135	US-10-052-586-488	US-10-036-342-74	US-09-799-777-68	US-10-036-041-74	US-10-001-876-210	US-09-864-761-47670	US-09-893-737-222	US-09-764-847-670	US-09-864-761-44740	US-09-864-761-48790	US-09-981-876-204	US-09-017-743C-105	US-09-017-743C-92	US-09-725-433-2	US-09-867-521-2	US-09-017-743C-70	US-09-466-320-12	US-09-466-320-20	US-09-888-721-21	US-09-466-320-11	US-09-466-320-19
896,	149,	Sequence 988, App	Sequence 1678, Ap	Sequence 135, App	Sequence 488, App	Sequence 74, Appl	Sequence 68, Appl	Sequence 74, Appl	Sequence 210, App	Sequence 47670, A	Sequence 222, App	Sequence 670, App	Sequence 44740, A	e 487	204,	Sequence 105, App	'n	Sequence 2, Appli		70, z	12,	Sequence 20, Appl	Sequence 21, Appl	Sequence 11, Appl	Sequence 19, Appl

ALIGNMENTS

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RESULT 2
US-09-821-883-5
; Sequence 5, Application US/09821883
; Patent No. US20020061310A1
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-883-23
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US-09-821-883-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 23
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30

CURRENT APPLICATION NUMBER: US/09/821,883

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: US 60/193,504

PRIOR PILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 555
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEO ID NOS: 30
SOFTWARE: FastSEO for Windows Version 4.0
SEO ID NO 5
LENGTH: BE 479
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APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
TITLE OF INVENTION: Compositions and Methods for Dendritic
TITLE OF INVENTION: Cell-Based Immunotherapy
FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/193,504 PRIOR FILING DATE: 2000-03-30
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Application US/09821883
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0; Mismatches
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Pred. No.
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RESULT 6 US-09-854-356-3

Sequence 3, Application US/09854356 Patent No. US20020177567A1 GENERAL INFORMATION:

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SOFTWARE: FastSEQ for Win SEQ ID NO 1
LENGTH: 645
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                            Query Match
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Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/92: CURRENT FILING DATE: 2001-08-01 PRIOR APPLICATION NUMBER: 60/225,433 PRIOR FILING DATE: 2000-08-15 NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ralph, Peter TITLE OF INVENTION: ANALYTICAL METHOD FILE REFERENCE: GENENT.066A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30
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APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                        199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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                259 NHSGICELHCPALVTYNTDTFES 281
                                                                     199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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NHSGICELHCPALVTYNTDTFES
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LSEQ for Windows Version
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100.0%; Pr
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Pred. No.
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5.4e-68;
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                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,504
PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Cell-Based Immunotherapy FILE REFERENCE: 7636-0022.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vidovic, Damir APPLICANT: Graddis, Thomas
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CURRENT FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
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NHSGICELHCPALVTYNTDTFES 300
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                                                                                                                                                               Score 83;
Pred. No.
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                                                                                                                                                                                                                                  SEQ ID NO 7
LENGTH: 712
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                     Query Match
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APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu fusion Proteins
FILE REFERENCE: 014058-009810PC
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
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CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
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CURRENT FILING DATE: 2001-03-30
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                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Laus, Reiner
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/117,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 697
TYPE: PRT
                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                    199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCCHEQCAAGCTGPKHSDCLACLHF 258
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199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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                                                                                                  Local
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                                                                              83; Conserv
                                                                                Conservative
                                                                                                                                                                             Description of Artificial Sequence: fusion of ECD and delta PD of human HER-2/neu
                                                                                              19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83; DB 10; Pred. No. 5.8e-68;
                                                                              0;
                                                                                                  Score 83;
Pred. No.
                                                                              Mismatches
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                                                                                                DB 9; L
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                                                                                                                 Length 712
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259 NHSGICELHCPALVTYNTDTFES

281

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; OTHER INFORMATION: Description of Artificial Sequence:fusion ; OTHER INFORMATION: of ECD and PD of human HER-2/neu US-09-854-356-6
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US-09-854-356-6
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                 SEQ ID NO 2
LENGTH: 1255
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SEQ ID NO 6
LENGTH: 919
                        Query Match
Best Local
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         Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09769508
Patent No. US20020155527A1
                                                                                                                                                                                                                       APPLICANT: STUART, SUSAN G.
APPLICANT: MONAHAN, JOHN J.
APPLICANT: LANGTON, BEATRICE CLAUDIA
APPLICANT: HANCOCK, MIRIAM E.C.
APPLICANT: CHAO, LORRINE A.
APPLICANT: BLUFORD, PETER
TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
FILE REFERENCE: BEBIO-111-C1
CURRENT APPLICATION NUMBER: US/09/769,508
CHERENT APPLICATION NUMBER: US/09/769,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
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APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                              CURRENT FILING DATE:
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CURRENT FILING DATE: 2001-05-09
                                                                                                                                                                      SOFTWARE: PatentIn Ver.
                                                                                             TYPE: PRT
ORGANISM: Homo
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ORGANISM: Artificial Sequence
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         83;
                        Similarity
         Conservative
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19.8%; 5c.
100.0%; Pr
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100.0%; Pr
'''a 0;
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     s; Score 83; DB; Pred. No. 9.8
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Pred. No. 7.5e-68;
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                      DB 9; L
                                      Length 1255;
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LOCATION: (990)..(1255)

OTHER INFORMATION: phosphorylation domain (PD)

NAME/KEY: DOMAIN

LOCATION: (990)..(1048)

OTHER INFORMATION: fragment of the phosphorylation domain, preferred

OTHER INFORMATION: portion (delta PD)

US-09-854-356-1
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Best Local Similarity
Matches 83; Conserv
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SEQ ID NO 1
                                                                                                         Sequence 2, App. Publication No.
                                                                                             GENERAL INFORMATION:
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APPLICANT:
                                                 APPLICANT: Hand-Zimmerman, Susan APPLICANT: Cheever, Martin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S.
TITLE OF INVENTION: HER-2/new Fusion Proteins
FILE REFERENCE: 014058-009810PC
                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
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LOCATION: (1)..(653)
OTHER INFORMATION: extracellular domain (ECD)
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LOCATION: (676)..(1255)
OTHER INFORMATION: intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: human HER-2/neu protein
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                                                                                                                                                                                                                                                                                                        199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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                                                                                                                           2, Application US/09930125
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               Lodes, Michael
                                   Foy, Teresa M.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                             US20020193329A1
                                                                                                                                                                                                                                                                                                                                                                         19.8%; 5-
100.0%; Pr
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Pred. No.
                                                                                                                                                                                                                              281
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, 9.8e-68;
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                                                  RESULT 15
US-09-811-115-3
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GENERAL INFORMATION:
                Sequence 3, Application US/098111115 Patent No. US20020035736A1
                                                                                                                                                                                                                                                                                   Query Match 19.8%; Score 83; DB 10; 19.8% Score 83; DB 10; 19.8% Fred. No. 9.8e-68; Matches 83; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-Erbb TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES FILE REFERENCE: GENENT.073A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall
APPLICANT: Mark Sliwkowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHDOS FOR THE THERAPY AND DIAGNOSIS TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES FILE REFERENCE: 210121.544
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/0 PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.8%; Score 83; DB ilarity 100.0%; Pred. No. 9. Conservative 0; Mismatches
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Search completed: January 14, 2003, 17:21:51 Job time: 16.3032 secs

APPLICANT: Erickson, Sharon APPLICANT: Schwall, Ralph

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; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-115-3
B.
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                                                                                 B
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 83; Conserv
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PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: King, Kathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENENT.034A
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                     199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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                                                                                 199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
                                       259 NHSGICELHCPALVTYNTDTFES 281
NHSGICELHCPALVTYNTDTFES 281
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Copyright (c) 1993 - 2003 Compugen
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US-09-630-155-2
US-08-422-734-1
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US-09-344-195-6
US-08-467-083-68
US-08-486-348A-68
US-08-486-545B-68
US-08-486-545B-68
US-08-466-545B-68
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Result No.

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259 N	199 CF 199 CF	Query Matc Best Local Matches	RESULT 1 US-09-630-155-2 US-09-630-155-2 Sequence 2, Application US/09630155 Patent No. 6414130 GENERAL INFORMATION: HER-2 BINDING A PAPLICANT: Doherty, Joni Kristin an TITLE OF INVENTION: HER-2 BINDING A NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: BAILT ON UNITER WRIGHT TREMAI COUNTRY: U.S.A. ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: PC COmpatible OPERATING SYSTEM: Windows95 SOFTWARE: Word CURRENT APPLICATION NUMBER: US/09/630, FILING DATE: 16-Jan-2001 CLASSIFICATION NUMBER: US/09/630, FILING DATE: 16-Jan-2001 CLASSIFICATION SYSTEM: WINDER: 47,309 REFERENCE/DOCKET NUMBER: 47,309 REFERENCE/DOCKET NUMBER: 49321 TELECOMMUNICATION INFORMATION: TELEPHONE: 206 628-7621 TELEFAX: 206 628-7621		22866666666666666666666666666666666666
NHSGICE	CKGSRCWGES	ch Simi 83;	2, Applice 1, Applice 2, Applice 1, Applice 1, Applice 1, Applice 1, Applice 1, Applice 1, Applice 2, Applice 1, Applice 2, Applice 3, Applice 3, Applice 4, Applice 4, Applice 4, Applice 5, Applice 6, Applice 7, Applice		155 155 155 155 155 155 155 155 155 155
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US-08-422-108-1
Sequence 1, Application Patent No. 6333169
GENERAL INFORMATION:
APPLICANT: Hudzia
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 08/355460
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TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
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APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                               178 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                  LENGTH: 624 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/0 FILING DATE: 15-APR-1993
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                                       Application US/08422734
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           STREET:
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; Patent NO. 5976546;
; GENERAL INFORMATION:
; APPLICANT: Laug, Re
; APPLICANT: Ruegg, C
; APPLICANT: Wu, Hong
; TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING LALL.
PRIOR APPLICATION DATA:
08/048346
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                          199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/04 FILING DATE: 15-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/3 FILING DATE: 13-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/4:
FTLING DATE: 14-Apr-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/3 FILING DATE: 19-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                            CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 237
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Similarity 100.0%; Pred. No.
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Palo Alto
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                                                                                                                                                                                     Application US/09146283
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              350 Cambridge Ave. Suite 250
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Ullrich,
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                                                                                                                 Ruegg, Curtis L.
                                                                                                                                   Laus, Reiner
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IBM PC compatible
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                                                                                Immunostimulatory Compositions
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                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                                                                                                                                                                                                             APPLICANT: I
APPLICANT: I
APPLICANT: V
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 782 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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CITY: Palo Alto
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                CLASSIFICATION:
                               APPLICATION NUMBER: FILING DATE: 03-DE
                                                                                                                                                        COUNTRY:
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INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
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                  03-DEC-1998
N: 536
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                                                                                                                                                                                                                                                              Immunostimulatory Composition and Method
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                                          US/08/579,823A
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RESULT 6
US-09-344-195-4
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GENERAL INFORMATION:
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                                                INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
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LENGTH: 782 amino acids
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TELECOMMUNICATION INFORMATION:
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INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MOLECULE TYPE: protein
                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                            NAME: Judge, Linda R. REGISTRATION NUMBER: 42,702
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/146,283 FILING DATE: 03-SEPT-1998
                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
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                TOPOLOGY: linear
                                     TYPE: amino acid
                                                                                                           TELEFAX: 650-324-0960
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                                                                                                                          TELEPHONE: 650-324-0880
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100.0%; Pr/
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Pred. No. 2.7e-71
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REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
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                                                                                            Query Match
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                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/414,417
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
   259
                               199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
                                             199 CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCCHEQCAAGCTGPKHSDCLACLHF 258
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CITY: S
                                                                                                                                                                                TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                    NAME: Sharkey, Richard REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                LENGTH:
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   NHSGICELHCPALVTYNTDTFES
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                                                                                                                                                                                                  1255 amino acids
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                                                                                          Conservative
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100.0%; Pr
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                                                                                                       Score 83;
Pred. No.
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   281
                                                                                         Mismatches
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US-08-414-417B-68
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                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5811098
Patent No. 5811098 5780031
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 68,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                   APPLICANT: Culouscou, Jean-Michel APPLICANT: Shoyab, Mohammed APPLICANT: Siegall, Clay B. APPLICANT: Hellstr m, Ingegerd APPLICANT: Hellstr m, Karl E. TITLE OF INVENTION: HER4 HUMAN RECENTATION: HUMAN RECENTATION: HUMAN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCE ADDRESS:

CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                      TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                CORRESPONDENCE
                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08484438
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                                                                                                                                                                                                                                                                                                         Plowman, Gregory D.
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                         ADDRESS:
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Edmonds
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; Pred. No. 4.2e-
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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of the Americas

New York

Floppy disk

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US-08-486-348A-68
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                                                                                                                                                                                                                              Sequence 68, Application US/08486348A Patent No. 5846538 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
-- Local Similarity
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CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/9
APPLICATION NUMBER: US 07/9
APPLICATION 24-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                             APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMINE RE.
TITLE OF INVENTION: FOR DIAGNO
                                                                                                                CORRESPONDENCE ADDRESS
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COMPUTER READABLE FORM:
                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                               TITLE OF INVENTION:
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 COUNTRY: US
*TP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unl
TOPOLOGY: unknown
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                                                                                                  ADDRESSEE:
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                                           Washington
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(212) 869-8864/9741
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                                                                           Seed and Berry LLP
00 Columbia Center, 701 Fifth Avenue
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                                                                                                                                               IMMUNE REACTIVITY TO HER-2/neu PROTEIN FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH HER-2/neu ONCOGENE IS ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.8%; Score 83; 100.0%; Pred. No.
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Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                   TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
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                                                                                          NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,6 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                     APPLICATION NUMBER: US/0:
FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sharkey, Richard G. REGISTRATION NUMBER: 32,629
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COMPUTER: II
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                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
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98104-7092
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                                                     (206) 622-4900
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                                                                                                          32,629
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US-08-468-545B-68
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RESULT
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                                                                                                                                                     Query Match
Best Local S
Matches 83
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GENERAL INFORMATION:
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Best Local
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Sharkey, Richard G
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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APPLICANT: Disis, Mary L.
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CITY: S
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                                                                                                                                                                                                                                                                                                                                                  NAME: Sharkey, Richard REGISTRATION NUMBER: 32
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                                                                  NHSGICELHCPALVTYNTDTFES 281
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FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
HER-2/neu ONCOGENE IS ASSOCIATED
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Pred. No
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4.2e-71;
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4.2e-71;
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                                                                                                                                                                     Description US/08466680B Patent No. 6075122
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                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cheever, Martinapplicant: Disis, Mary L.
APPLICANT: Disis, Mary L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT:
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REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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                                             CORRESPONDENCE ADDRESS
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ATTORNEY/AGENT INFORMATION:
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                STREET:
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TOPOLOGY: linear
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Seattle
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             6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                            Cheever, Martin A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huston,
                                Seed and Berry LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edmund R. Pitcher, Testa, Hurwitz, & Thibeault change Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biosynthetic Binding Protein for Cancer Marker
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                                                                                                                                                                                                                                                                                                                                                                                                                          19.8%;
                                                            IMMUNE REACTIVITY TO HER-2/neu PROTEIN
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
HER-2/neu ONCOGENE IS ASSOCIATED
69
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Pred. No.
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RESULT 15
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08421356
Patent No. 5783404
GENERAL INFORMATION:
                              REFERENCE/DOCKET NUMBER: A-327
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 68:
                                                                                                                                                                                            ZIP: 91340-1/0,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/421,356
                                                                                                                                                                                                                                                                                                                                                                   STREET: 1840 CONTROL Thousand Oaks
STATE: California
                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
TOPOLOGY: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TENGTH: 1255 -
TYPE: amino acid
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                                                                                                                                                                                 FILING DATE: CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
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y Match 12.4%; Score 52; DB 1; L
Local Similarity 100.0%; Pred. No. 2.2e-42;
hes 52; Conservative 0; Mismatches 0;
                                                                     Length 97;
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Search completed: January 14, 2003, 17:15:48 Job time: 29.9237 secs

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:

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Human p68HER-2 gen.
Human truncated HE
Human p68HER-2 gen
                                                                                                                                                                                       Description
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AAB85458	AAE12130	AAY92620	AAY84780	AAB21198	AAW92406	AAW01111	AAU98923	AAB21208	AAY44993	AAM51148	AAB21203	AAW19764	AAM51149	AAB21204	AAE13111	AAE13109	AAM51145	AAB21200	AAB61593	AAB60408	AAE13110	AAE13108	AAE13112	AAE13120	AAY97240	AAE09203	AAE09213	AAE09205	AAE09204	AAE09216	AAE09215	AAE09214	္က	AAE09200
Human HER-2/neu pr	tyrosine k	Human heregulin 2	Amino acid sequenc	HER-2/neu	HER-2/neu o	HER-2/neu protein.	breast car		Ħ	/neu extrac	`	GM-CSF immun	/neu extrac	HER-2/neu f			Human Her-2/neu on	cellula	ErbB2	ErbB2 c		HER500	HER300-rGM-	hum	ated HER-2	p68HER-2	p68HER-2	p68HER-2	p68HER-	p68HER-2	p68HER-2	p68HER-2	р68нER-2	Human p68HER-2 gen

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/label= Unknown /note= "Encoded by WCC" Misc-difference 345 /label= Unknown	Misc-difference 125 //note= "Represented as Agn in the sequence shown in the specification" Misc-difference 342	/label= ECDIIIa /note= "Extracellular domain IIIa" Misc-difference 124 /note= "Represented as Agn in the sequence shown in the specification"	Homo sapiens. Key Location/Qualifiers Region 1340 Note= "Identical to N-terminal region of p185HER-2" Domain 341419	HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin; solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2; ECDIIIa

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Best Local S
Matches 294
                                                                                                                                                              The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of
                                                                                  Sequence
                                                                                                                        p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify
                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                N-PSDB; AAD15844
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                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                           2001-529934/58
                                                                                                                                                                                                                                                            8; Page 53-54; 61pp; English.
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                                                                                                      ECDIIIa
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                                                            Length 419;
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                                     16-FEB-2001; 2001WO-US05327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE09208 standard; Protein; 419
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                                                                                                                                                                /label= Unknown
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in the specification"
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in the specification"
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16-FEB-2000; 2000US-0506079

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised cantibody, Herceptin, at an affinity of at least 10.8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product CC of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. CT The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise CC the HER-2 receptor. The peptides which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify CC solid tumours. The present sequence is human p68HER-2 generic protein CC containing ECDIIIa variant sequence.

CC Note: The present sequence is not shown in the specification but is certain particularly (AAE09181).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                          Human; tumour; endothelial growth factor receptor; EGFR; herstatin; HER-2 receptor tyrosine kinase; squamous cell colon; glial cell tumour; cell growth.
                                                                                                                                                                 AAE20348;
                                                                                                      Human
                                                                                                                                   18-JUN-2002
                                                                                                                                                                                               AAE20348 standard; Protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide, which binds treatment of hard tumors
                                                                                                                                                                                                                                                                                                                                                                                                           GPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCVTACPYNKLS
                                                                                                                                                                                                                                                                      VLSFLRPSWDXVSAFYSLPLAPLDPTSVXISPVSVGRGXDPDAHVAVXLSRYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID 185
                                                                                                                                                                                                                                                                                                                                                                                          GPKHSDCLACLHENHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCVTACPYNKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT
                                                                                                      truncated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419
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                                                                                                                                  (first entry)
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                                                                                                      HER2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.8%; Score 284; DB 22; 100.0%; Pred. No. 3.2e-259; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                        cytostatic;
carcinoma;
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                                                                                                                    Query Match
                                                                                               Matches
                                                                                                                                                                The present invention relates to a method for treating a solid tumour characterised by endothelial growth factor receptor (EGFR) expression. The method involves administering an agent that binds to an extracellular domain (ECD) of EGFR. The invention also relates to a naturally occurring inhibitor of HER-2 receptor tyrosine kinase called herstatin. The coexpression of herstatin with p185HER2 causes a striking reduction in cell growth that corresponds with suppression of p185 autophosphorylation. The method or a pharmaceutical composition is useful for treating a solid tumour (selected from squamous cell carcinoma, lung carcinoma, colon carcinoma and g1ial cell tumour) characterised by EGFR expression. The present sequence is human truncated HER2 protein that lacks transmembrane and intracellular domains.
                                                                                                                                                                                                                                                                                                                                                        Treating solid tumor characterized by expression of endothelial factor receptor, involves administering recombinant herstatin to binds to extracellular domain of the endothelial growth factor.
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                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                        Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Clinton GM
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                        186
                                                126
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                                                                                                          Local Similarity
TNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT
                                                          TTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID 185
                                               TTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIV OREGON HEALTH SCI
                                                                                                                                                                                                                                                                                                                        Page 78-80;
                                                                                                                                             419 AA;
                                                                                             67.8%;
ilarity 100.0%;
Conservative
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                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ala,
                                                                                                        3.2e-259;
                                                                                                                     DB 23;
                                                                                                                   Length 419;
                                                                                              Indels
                                                                                             0;
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                 growth
                      245
                                               185
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RESULT 4
AAEC 9212
ID AAEC
XX AAEC
XX HUMA
XX HERR
KW SOLL;
KW SOLL;
KW P68+
XX HOMC
FT Mis
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  WPI;
                                        Clinton G,
                                                                                                                        16-FEB-2000;
                                                                                                                                                              16-FEB-2001;
                                                                                                                                                                                                        23-AUG-2001
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                                                                                                                                                                                                                                              WO200161356-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P68HER-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HER-2; herstatin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001
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                                                                                (UYOR-)
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  2001-529934/58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSFLRPSWDXVSAFYSLPLAPLDPTSVXISPVSVGRGXDPDAHVAVXLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLSFLRPSWDXVSAFYSLPLAPLDPTSVXISPVSVGRGXDPDAHVAVXLSRYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; cancer; polymorphism; cytostatic; gene therapy; R-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p68HER-2 generic
                                                                             UNIV OREGON HEALTH SCI.
                                        Henner WD,
                                                                                                                      2000US-0506079.
                                                                                                                                                              2001WO-US05327
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124
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345
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                                                                                                                                                                                                                                                                                      substituted
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                                                                                                                                                                                                                                                                                    note= "p68HER-2
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in the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identical to N-terminal region of p185HER-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
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Asn"
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New
the
                                                                                   Example 11; Page -; 61pp; English.
                                                                                            polypeptide, which binds to the treatment of hard tumors -
                                                                                                extracellular domain
                                                                                                of HER-2 for
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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated possible. The transcript is a truncated HER-2 protein designated possible. The contains ECD I I of the pl85HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify anticid time. solid tumours. The present sequence is human p68HER-2 containing ECDIIIa variant sequence.
Note: The present sequence is not shown in the specifi derived from p68HER-2 generic sequence (SEQ ID NO:2) s sequence from p68HER-2 generic sequence listing (AAE09181). specification NO:2) shown in generic n but is protein

Sequence 419 Ä

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Best Local S
                                                                                                                                                                               126 TTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID 185
                                               306
                                                                                                                                                             186
   366
                        366
                                                                     306
                                                                                            246
                                                                                                                246
                                                                                                                                        186
                                                                                                                                                  TNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT
GPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCVTACPYNKLS
                                           TDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGXHSXXPRPAAVPVPXRXQPXPAHP
                                                          TDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGXHSXXPRPAAVPVPXRXQPXPAHP
                                                                                          GPKHSDCLACLHENHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCYTACPYNKLS
                                                                                                                                     TNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT
                                                                                                                                                                                                                              287;
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                           66.3%; S ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                           Score 278; DB; Pred. No. 1.5
0; Mismatches
                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                        .5e-253;
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                 Length 419;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                            0
                                                                                                                                                                                                                            Gaps
                                                                   365
                                                                                                               305
                                              365
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                                                                                                                                     245
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AAE09211
XX
AAE
XX
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AC
AAE
DT
15-1
XX
KW
HER
KW
SO1.
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Domm
                                                                                                                                                                                                                     RESULT
                                                                                                     HER-2;
solid 1
                    Domain
                                       Region
                                                                     Homo sapiens
                                                                                         P68HER-2;
                                                                                                                                   Human
                                                                                                                                                       15-NOV-2001
                                                                                                                                                                            AAE09211
                                                                                                                                                                                               AAE09211 standard;
                                                                                                                                                                                                                    σ
                                                                                         tumour; cance
R-2; ECDIIIa;
                                                                                                                                   p68HER-2
                                                                                                            herstatin; antagonist; extracellular domain; ECD; Herceptin;
                                                                                                                                                     (first entry)
                                                                                                     cancer;
                                                                                                                                   generic
                   /note= "Identical to N-terminal region
341..419
                                                 Location/Qualifiers
                                                                                                                                                                                               Protein;
                                                                                                   polymorphism; cytostatic;
                                                                                                                                  protein variant 9.
                                                                                                                                                                                                419
                                                                                                                                                                                               À
                                                                                                   gene
                                                                                                   therapy;
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/note= "Extracellular domain IIIa variant"

ECDIIIa_variant

of p185HER-2"

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QΥ
                                                                                                                                                        The invention relates to novel HER-2 (herstatin-2) antagonist

particularly a polypeptide that binds to the extracellular domain (ECD)

of HER-2 at a site that is different from the binding site of humanised

antibody, Herceptin, at an affinity of at least 10^8. The present

invention is based upon the initial discovery of an alternative HER-2

mRNA transcript with 274 bp insert of intron 8. The translation product

of the alternative transcript is a truncated HER-2 protein designated

p88HER-2 which lacks the transmembrane and intracellular domains of

p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa.

The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise

the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the

nucleic acids encoding these are useful to treat, diagnose and identify

solid tumours. The present sequence is human p68HER-2 generic protein

containing ECDIIIa variant sequence.
                                                     Query Match
Best Local
                                          Matches
                                                                                                                  Note: The present sequence is not shown derived from p68HER-2 generic sequence sequence. listing (AAE09181).
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                              Example 11;
                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2001; 2001WO-US05327
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126 TTPVTGASPGGLRELQLRSLTECLKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLID 185
                                                                                                                                                                                                                                                                                                                                                                                       polypeptide, which binds to the extracellular domain of \ensuremath{\mathsf{HER}\text{--}2} treatment of hard tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                               2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ģ
                                                     Similarity
                                                                                            419
                                                                                                                                                                                                                                                                                                                                                             Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henner WD,
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "p68HER-2;
substituted with I
e 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= Unknown
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                                  64.4%; sc.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Represented as specification"
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                                                 Score 270; DB 22; Pred. No. 5.2e-246;
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                                                                                                                                 not shown in the specification but is sequence (SEQ ID NO:2) shown in the
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          generic sequence (AAE09181) Xaa
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                                       0;
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                                                                Length 419
                                       Indels
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RESULT 6
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solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
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                                                                                       /note= "p68HER-2 substituted with
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Homo sapiens

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Best Local Similarity
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HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                            Human
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                                                                                                                                                         AAE09209 standard;
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                                                            P68HER-2
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100.0%; PY
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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 bit contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify
             solid tumours. The present sequence is human p68HER-2 containing ECDIIIa variant sequence. Note: The present sequence is not shown in the specifiderived from p68HER-2 generic sequence (SEQ ID NO:2) s
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Best Local
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                   Misc-difference
                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human p68HER-2 generic protein variant (Arg371Ile).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLSFLRPSWD 375
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                                                                                                                                                                                                                                               /label=
346
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in the specification"
125
                   /note= "p68HER-2
substituted with
376
                                                                                                                                                                                                                                                                                        /label= Unknown
345
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                                                                                                                                           abel-
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Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                           sequence (AAE09181)
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                                                                                                                                                                                                                                                                                                                                                                                                                               parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant"
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                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
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                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised cantibody, Herceptin, at an affinity of at least 10°8. The present convention is based upon the initial discovery of an alternative HER-2 coments at truncated HER-2 protein designated to fithe alternative transcript is a truncated HER-2 protein designated coments. The present sequence and intracellular domains of p185HER-2 which lacks the transmembrane and intracellular domains of cp185HER-2 which lacks the transmembrane and intracellular domains of cp185HER-2 but contains ECD I I I of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise concluded a containing these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.

Note: The present sequence is not shown in the specification but is containing ECDIIIa variant sequence (SEQ ID NO:2) shown in the sequence listing (AAE09181).
                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide, which binds to the extracellular domain of HER-2 the treatment of hard tumors - \  \  \,
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                                                                                                                                                                                                                                                                                            Local Similarity
mes 245; Conserv
                                                                                                                                                                                                                                  VLSFL 370
                              VLSFL 370
                                                                       TDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGXHSXXPRPAAVPVPXRXQPXPAHP
                                                                                                               GPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESCPNPEGRYTFGASCVTACPYNKLS
                                                                                                                                                                        TDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGXHSXXPRPAAVPVPXRXQPXPAHP
                                                                                                                                                                                                                                                                                                                                                        419
                                                                                                                                                                                                                                                                                            57.0%; Score 239; Dilarity 100.0%; Pred. No. 8.1 Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                           8.8e-217;
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for

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Gaps

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185 185

245

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305

365

RESULT 9
AAE09207

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particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10'8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product
                                                                                                                                                                                                                                                                                                                                                                                                                    HER-2;
solid t
                                 The invention relates to
                                               Example
                                                                                           Clinton
                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                               23-AUG-2001
                                                                                                                                                                               Misc-difference
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                                                                                                                     16-FEB-2000;
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                                                                                                        (UYOR-)
                                                          polypeptide, which treatment of hard t
                                                                              2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                    tumour;
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                                                                                                        VINU
                                             11; Page -;
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                                                                                           Henner
                                                                                                        OREGON
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413
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346
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345
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tumors
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of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               solid tumours. The present sequence is human containing ECDIIIa variant sequence.
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                                                                                                  particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8: The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 protein
                                                                                  Sequence
                                                                                                                                                                                                                                       The invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                            Claim
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treatment of hard tumors
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RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cin; antagonist; extracellular domain;
cancer; polymorphism; cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Represented as
in the specification"
342
                                                                                                                                                                                                                                                                                                                                                                                 substituted with 358
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341 419
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in the specification"
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/note= "Extracellular d
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                                                                                                                                                          /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                    note= "p68HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .abel= Unknown
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                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                         Unknown
                                                                                                                                                                                                                                                                                Unknown
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16-FEB-2000; 2000US-0506079.

(UYOR-) UNIV OREGON HEALTH

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Note: The present sequence is not shown in the specification but is derived from p68HER-2 generic sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
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the
  Domain
                                                                                                                                   P68HER-2;
                                                                                                                                                        HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                    AAE09206 standard;
                                        Region
                                                                                               Homo sapiens
                                                                                                                                                                                                                                                       15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence listing (AAE09181).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNRSRACHPCSPCCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCT
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                                                                                                                                                                                                                  p68HER-2
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                                                                                                                                   bur; cancer; polymorphism; cytostatic;
ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 AA;
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                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                generic protein variant 4.
1..340 /note= "Identical to N-terminal region of p185HER-2" 341..419
                                                                                                                                                                                                                                                                                                                                    Protein;
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Pred. No.
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1.8e-205;
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Query Match Best Local : Matches 230;

Similarity

100.0%;

Score 227; DB 22; Pred. No. 1.8e-205; Mismatches

Length 419;

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Gaps

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Conservative

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Sequence

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                                 particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify containing ECDIIIa variant sequence. Solid tumours. The present sequence is human p68HER-2 generic protein CC containing ECDIIIa variant sequence (SEQ ID NO:2) shown in the
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                                                                                                                                                                                                                                       The invention relates to novel HER-2 (herstatin-2) antagonist
                                                                                                                                                                                                                                                                    Example 11; Page -; 61pp; English
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-529934/58
                                                                                                                                                                                                                                                                                                                                                               Clinton G,
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                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-2000; 2000US-0506079.
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                         listing (AAE09181).
                                                                                                                                                                                                                                                                                                                                                                 Henner WD,
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413
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376
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/note= "Extracellular domain IIIa variant"
124
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in the specification"
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Region
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                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    solid tumour; cancer; polymorphism; cytostatic;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                            HER-2; herstatin;
solid tumour; can;
                                                                                                                                                                                                                                                                                                                                                                                                    Human p68HER-2 generic protein variant 13.
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the specification"
e 125
                                                                                                                                  /note= "p68HER-2;
substituted with C
= 358
                                                                                                                                                           /label= Unknown
357
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                                                                                                                                                                                                                                               /note= "Represented
                                                                                                                                                                                                                                                                                                                 note= "Identical to N-terminal region of p185HER-2"
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                        'label=
                                                        'label=
                                                                                                                                                                                                                                                                                                  /label= ECDIIIa_variant
                                                                                                                                                                                                                                                                                                                                                                                     antagonist; extracellular domain;
                                                                                         abel-
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RESULT 14

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              solid tumours. The present sequence is human p68HER-2 containing ECDIIIa variant sequence. Note: The present sequence is not shown in the specifiderived from p68HER-2 generic sequence (SEQ ID NO:13) sequence listing (AAE09183).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                           HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Homo sapiens

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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10%. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated of the alternative transcript is a truncated HER-2 protein designated
                            p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify
        solid tumours. The present sequence is human containing ECDIIIa variant sequence.
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                                                                                                                                                                               polypeptide, which binds treatment of hard tumors
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/note= "Extracellular domain
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solid tumour; cancer; polymorphism; cytostatic; gen-
p68HER-2; ECDIIIa; variant.
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                                                   -difference
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376
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                                                                                                                                                                                                                                                                                                                                            The invention relates to novel HER-2 (herstatin-2) antagonist CC particularly a polypeptide that binds to the extracellular domain (ECD) CC of HER-2 at a site that is different from the binding site of humanised CC antibody, Herceptin, at an affinity of at least 10°8. The present CC invention is based upon the initial discovery of an alternative HER-2 CC mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated CC p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein Containing ECDIIIa variant sequence.

Note: The present sequence is human p68HER-2 generic protein the sequence listing (AAE09183).
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186
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Search completed: January 14, Job time: 54.8474 secs

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ol4596 homo sapien
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O67814 aquifex aeo
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Clinton G.M., Adelman J

Doherty J.K., Clinton G.M., Adelman J

Submitted (SEP-2000) to the EMBL/GenB

EMBL, AF177761, AAD56009 2; -

InterPro; IPR000494; EGFR_L_domain.

InterPro; IPR002174; Furin-like.

Pfam; PF01030; Recep_L_domain; 1.

SMART; SM00261; FU; 1.
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Q9UK79; O1-MAY-2000 (TTEMBLrel. 13,
Q1-MAR-2001 (TTEMBLrel. 16,
Q1-JUN-2002 (TTEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doherty J.K., Bond C., Jardim A., Adelman J.P., Clint "The HER-2/neu receptor tyrosine kinase gene encodes autoinhibitor.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=99415951; PubMed=10485918;
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X Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamura K., Kaneko T., Nakamura M., Ishikawa A., Kawashima K., Kaneko A., Iriguchi M., Ishikawa A., Kawashima K., Kaneko A., Iriguchi M., Ishikawa A., Kawashima K., Kaneko T., Nakasawa M., Yamani M., Yamani
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                                                                                                                                                                                         cyanobacterium Anabaena sp. strain DNA Res. 8:205-213(2001). EMBL; AP003582; BAB72295.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
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"Complete genomic sequence of the
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'and multivitamin transporter (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2620 MW;
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100.0%; Pr
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      8.98;
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Nostocales;
                                                                    MW.
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Last
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Pred. No
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      Score 7;
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                                                          proteome.
8E01290F333B1B7A CRC64;
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annotation
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n PCC 7120.";
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Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
2A Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
2A Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
2A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
2A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
2A Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
2A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
2A Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
2A Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
2B Trull Length cDNA of gene MUKII.15/AT5g04830 (GI:9758458).";
2B Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
2B EMBL; AB008271; BAB08987.1; -.
2B EMBL; AF360335; AAK28632.1; -.
2B EMBL; AF360335; AAK28632.1; -.
2B EMBL; AF360335; AAK28632.1; -.
2B EMBL; AF360370; AAK393747.1; -.
2B EMBL; AF051070; AAK393747.1; -.
2B EMBL; AF051070; AAK393747.1; -.
                                                                                                                                                                                                                        Query Match
Best Local :
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Matches
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STRAIN=COLUMBIA;
MEDLINE=98162728; PubMed=9501997;
MEDLINE=98162728; Raneko T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence)
01-DEC-2001 (TrEMBLrel. 19, Last annotain Hypothetical 20,3 kDa protein.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidops
Sequence features of the regions
physically assigned P1 clones.";
DNA Res. 4:401-414(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis A.; "Full Length cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                            66 SAFYSLP
                                                                                                                                                     38 SAFYSLP
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene MUK11.15/AT5g04830 to the EMBL/GenBank/nnp.
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                                                                                                                                                                                                                        Score 7;
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Mismatches
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245 AA
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21;
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J databases.
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J.R.,
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Matches 7
                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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TISSUE-SALIVARY GLAND;

Verma R.S., Elwood P.C.;

Verma R.S., Elwood P.C.;

"Identification of a homologous cDNA to folate r.salivary gland.";

submitted (APR-1997) to the EMBL/GenBank/DDBJ da
EMBL; AF000380; AAB81937.1; -.

InterPro; IPR004269; Folate_rec.

Pfam; PF03024; Folate_rec; 1.

SEQUENCE 245 AA; 26268 MW; BA36B7DB95FC0E20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-IMRU 3570;
STRAIN-IMRU 3570;
Campelo A.B., Gil J.A.;
"Cloning and characterization of a gene cluster from Streptomyces griseus IMRU 3570 involved in candicidin production.";
griseus IMRU 3570 involved in candicidin production.";
                                                                                                                                                                                                                                                                                                                                                                                             PF01051; ABC2 membrane;
PRINTS; PR00164; ABC2 TRNSPORT
PROSITE; PS00890; ABC2 MEMRDANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thesis (2000), Department of Microbiologia, Universidad EMBL; AJ300302; CAC22119.1; -. InterPro; IPR000412; ABCtranprtr2.
                         Q9U3E1
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-IMRU 3570;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANRB
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                                                                                                                                                          PRPAAVP 8
                                                                                                                                                                                                                                                               Similarity 7; Conserv
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                      PS00890; ABC2_MEMBRANE; UNKNOWN_1.
268 AA; 27945 MW; C621E71DE2EFF7B4 CRC64;
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                               Score 7; DB 2; Pred. No. 30; 0; Mismatches
                                                                                                                                                                                                                                                                 0;
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                         PRT;
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Matches 7
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QBUEF8;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S.,
Goodner B., Goldman B.S., Cao Y.,
Qurollo B., Goldman B.S., Vaudin M.,
                                                                                                                                                                                                                                                         Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo I. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo Raymond S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
SMARR; SM00353; HLH; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                     "The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Rhiz
NCBI_TaxID=176299;
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HSSP; P36956; LAM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                Science
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                                                                                                                                                                                                                                     genome
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                                                                                                                                                                                294:2317-2323(2001).
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Mismatches
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              , Miller N., Blanchard M. Askenazi M., Halling C., Iartchouk O., Epp A., Li
                                                                                                                                                                                                                                     engineer
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Best Local
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STRAIN-A3(2) / M145;

Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
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Flanagan C.
Cielo C., S
                                                      "Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
Nature 417:141-147(2002).
                                                                                                                                                                                                                                         "A set of ordered cosmids and a detailed genetic at the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
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Saunders D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
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"Genome sequence of the plant
Agrobacterium tumefaciens C58.
Science 294:2323-2338(2001).
                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                           Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2000)
                                                                                                                                                                                                                                                                                                                                                         Cerdeno
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                  MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
 y Match
Local :
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                                           AL353862; CAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAAVPVP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAAVPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE009135; AAL42798.1;
AE008101; AAK87570.1;
                                                                                                                                                                                                                                                                                                                                                          Α.
Similarity
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                                  416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                        Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
                                                                                                                                                                                                                                                                                                                                                                                                to +
                                  43715 MW;
8.9%;
100.0%;
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100.0%;
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f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence upo
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                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
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Score 7; I
                                                                                          the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
DED360C24024E93B CRC64;
                                  92CEAE6017968445 CRC64;
                                                                                          model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacteridae;
 DB 16;
. 43;
                                                                                       actinomycete Streptomyces
                                                                                                                                                                                                                                                      genetic and
hromosome.";
                                                                                                                                                                                                                                                                                     Eichner
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         Length 416;
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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01-AUG-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                              01-MAR-2002
01-MAR-2002
01-MAR-2002
SEQUENCE
                                EMBL; AJ399793;
                                                                  melanogaster.";
Submitted (JAN-2000)
                                                                                                                                       STRAIN=K13;
                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                           Pterygota; N
Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                  Q8WQ63;
                                                                                                                                                                                                                                                                                                                                                                                  Q8WQ63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000768; AAC07778.1;
InterPro; IPR002937; Amino_c
InterPro; IPR000205; NAD_bii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graham D.E., Overbeek R., Feldman R.A., Short J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex aeolicus.
Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               067814
                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                            Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMs; TIGR00562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deckert G., Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protoporphyrinogen
                   NON_TER
                                                                                                                       Zangerl B.
                                                                                                                                                                                                                                                                               ZESTE
                                                                                                                                                                                                                                                                                            Zeste protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEMG OR AQ_
                                                                                                     "Evidence
                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004572; Proto_IX
Pfam; PF01593; Amino_oxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 VLSFLRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 VLSFLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                     for selection
                                                                                                                                                                                                      Neoptera; Endopte
a; Drosophilidae;
 469
                                                                                                                                                                                                                      Metazoa; Arthropoda; Trac
Neoptera; Endopterygota;
                                                                                                                                                                                                                                                            melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
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                   469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
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 Ā
                                                   CAC81400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.V., Gaasterland T., Young
eek R., Snead M.A., Keller N
t J.M., Olson G.J., Swanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxidase.
 51012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD_binding.
Proto_IX_ox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aquificales; Aquificaceae; Aquifex
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                                                                                                                                                                                                                                                                                                            20,
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07,
21,
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Last sequence up
Last annotation
                                                                   EMBL/GenBank/DDBJ
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Last annotation update
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                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                    natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
 5F3399F575C6CE24 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ED5F2B1BCD1DEEF7
                                                                                                                                                                                                                                        Tracheata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                          Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T., Young W.G., Y., Keller M., Aujay M. Swanson R.V.;
                                                                                                    population
                                                                                                                                                                                                                                                                                                                                                                                  469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1
                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                      Hexapoda; Inse
a; Brachycera;
                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                   databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                  of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                        Insecta;
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                                                                                                                                                                                                                        Muscomorpha;
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Huber
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POR REPORT OF THE PROPERTY OF 
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Q8WPA9
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Best Local Similarity
""" Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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01-MAR-2002 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20,
Zeste protein (Fragment).
ZESTE.
Submitted (JAN-2000) to the EEMBL; AJ399747; CAC81411.1; EMBL; AJ399748; CAC81412.1; EMBL; AJ399749; CAC81413.1; EMBL; AJ399751; CAC81415.1; EMBL; AJ399756; CAC81421.1; NON_TER
                                                                                                                                                                                                                                                                                                                              Q8WP54;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN 2000) to the EMBL; AJ399788; CAC81395.1; EMBL; AJ399795; CAC81402.1; EMBL; AJ399798; CAC81405.1;
                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musce Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08WPA9;
01-MAR-2002
                                                                                                                  melanogaster.
                                                                                                                                                    Zangerl B.
                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-ND6, ND7, N
                                                                                                                                                                                                                                                                                                    Zeste protein (Fragment).
ZESTE.
                                                                                                                                                                                                                                                                                                                                                                                                  Q8WP54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Evidence for selection in a natural population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zangerl B.
                                                                                                                                     Evidence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAAVPVP 368
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                                                                                                                                     for selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469
469 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K19, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%;
ilarity 100.0%;
Conservative
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                                  "Evidence for selection in a melanogaster.";
Submitted (JAN-2000) to the EMBL; AJ399791; CAC81398.1;
                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/001,876
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,186
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: DEX-0285
                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.53

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.52

OTHER INFORMATION: SWISSPROT HIT: Q13563, EVALUE 2.00e+00

OTHER INFORMATION: EST_HUMAN HIT: BF570694.1, EVALUE 4.00e-16
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Ali, Shujath
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US-09-864-761-41953
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Best Local 9
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SEQ ID NO 41953
                                                                      Matches
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
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OTHER INFORMATION:
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OTHER INFORMATION:
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24
                                47 PLSPTS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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                                                                  7.6%; ilarity 100.0%; Conservative
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: EXPRESSED IN PLACE:
: EXPRESSED IN HEART:
: EXPRESSED IN ADULT
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David K.
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DIN HEART, SIGNAL = 3.2
ED IN ADULT LIVER, SIGNAL = 3
ED IN BRAIN, SIGNAL = 3.6
ED IN LUNG, SIGNAL = 3.7
ED IN HELA, SIGNAL = 3.9
ED IN FETAL LIVER, SIGNAL = 3
ED IN BONE MARROW, SIGNAL = 2
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Pred. No. 13;
0; Mismatches
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O. 13;
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: X
US-09-764-887-226
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LOCATION: (48)
OTHER INFORMATION:
US-09-764-869-1118
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US-09-925-301-1470
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: Sequence 1118, Application US/09764869

: Patent No. US20020061521A1
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Best Local Similarity
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                             GENERAL INFORMATION:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA113
                                        Sequence 1470, Application US/09925301 Patent No. US20020052308A1
                                                                                                                                                                                  Matches
                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult NUMBER OF SEQ ID NOS: 658
                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: >
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids,
FILE REFERENCE: PC007
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TYPE: PRT
ORGANISM: Homo s
 APPLICANT: Rosen et
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 2442
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b; Pred. No. 29;
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Proteins and Antibodies
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                       Matches
                            CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
                                                                                   APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20020119522A1el Human Ion Channel-Related Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                    APPLICANT: Friddle, Carl Johan APPLICANT: Gerhardt, Brenda
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                 NUMBER OF
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LOCATION: (153)
OTHER INFORMATION:
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LOCATION: (141
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LOCATION: (152
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les 6; Conserv
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Best Local Similarity
Watches 6; Conserve
                                   ; ORGANISM: homo sapiens
US-10-024-579-12
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                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 264
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexand
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APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-0SA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
Query Match
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LENGTH:
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                                                                                                                                                                            APPLICANT: Gerhardt, Brenda
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. US20020119522Alel Human Ion Channel-Related Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
CURRENT APPLICATION NUMBER: US/10/024,579
CURRENT FILING DATE: 2001-12-18
                                                                                                                                PRIOR APPLICATION NUMBER: US 60/258,595
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 17
                                                                    TYPE: PRT
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87 VLSFLR 92
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100.0%; Pr
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Pred. No.
Score 6;
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Length 264;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-23
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
                                   NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
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Best Local Similarity 100.0%;
Matches 6; Conservative
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                                                                                          CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
CURRENT PPLICATION NUMBER: 09/800,198
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
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CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
                                                                                                                                                                                        APPLICANT: Mezes, Peter S
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
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TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding Same
FILE REFERENCE: 15966-697 CIP
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                                                                                                                                                                                                                                                                                                                                   PPLICANT: Vernet,
ORGANISM: Homo sapiens
                            ENGTH: 267
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20 LPLAPL 25
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Mishra, Vishnu
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Shimkets, Richard A
Herrman, John L
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Herrman, John L
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US-09-808-602-25

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RESULT 13
US-10-041-006A-7
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; LENGTH: 283
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-024-579-10
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA encoding the novel human serine TITLE OF INVENTION: protease T FILE REFERENCE: ORT-1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hilbun, Erin
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20020119522A1el Human Ion Channel-Related Proteins
TITLE OF INVENTION: and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0274-USA
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: Andrade-Gordon, Patricia
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                                                                                                                                LENGTH: 290
TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 1997-08-26
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60/073612

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APPLICANT: Darrow, Andrew
APPLICANT: 01, Jian-Shen
TITLE OF INVENTION: DNA encoding the novel human serine
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CURRENT FILING APPE: 200-10-7

NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 290
TYPE: PRT
ORGANISM: Homo sapiens
US-10-040-655-7

Query Match
ORGANISM: Homo sapiens
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4 mus musculu
5 homo sapien
8 pinus thunb
0 zea mays (m
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6 gallus gall
7 mus musculu
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P73881 synechocyst	Q45618 bacillus st	٠.		P23092 cas-ns-1 mu	Q01331 erwinia her		P21687 pantoea ana	Q98fyl rhizobium l		P41903 saccharomyc	P20186 streptomyce

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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
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Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
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Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
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Wohldman D.
                                                                                                                                                                                        SEQUENCE
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-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTOR S. STRONGEST, TO TRANSCRIPTION FACTOR AP-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                           WormPep; F58A4.7; CE01018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z22179; CAA80167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                 Apportmentical protein; Transcription regulation;
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                                       APLSPTS 52
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PF00010; HLH; 1.
                                                                                        Similarity 7; Conser
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                                                                                           Conservative
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54
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                                                                                                            8.9%;
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Last annotation updat
protein F58A4.7 in ch
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RX MEDILINE-20196006; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Lip P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basca M., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Sensam D.A., Bahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Davies P., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Larvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M., Retchum K.A.,
RA Hostin D., Houston K.A., Nixon K. Reticon J.A., Netchum K.A.,
RA Hostin D., Rodrader T., Wolland T.J., Will D., Nelson D.L.,
RA Hostin D., Rodrader T., Wolland T.J., Will D., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rount S.M., Pittman G.S., Pan S., Pollard J., Wang S.H., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z OR EG:BACH59J11.3 OR CG7803.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eukaryota; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZEST_DROME STANDARD; PRT; 574 AA PO9956; Q24596; Q3V3F1; 01-MAR-1989 (Rel. 10, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence and structural analysis Drosophila melanogaster."; Mol. Gen. Genet. 211:121-128(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87718538; PubMed=3582372; Pirrotta V., Manet E., Hardon E., Bickel S.E., Benson "Structure and sequence of the Drosophila zeste gene." EMBO J. 6:791-799(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 9:2959-2967(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Self-association of the transvection effects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bickel S.E., Pirrotta V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90361011; PubMed=2118108;
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Hey J., Kilman R.M.;

"Population genetics and phylogenetics of DNA sequence variation genetics and phylogenetics of DNA sequence variation in the Drosophila melanogaster species complex.";

Mol. Biol. Evol. 10:804-822(1993).

-I- FUNCTION: INVOLVED IN TRANSVECTION PHENOMENA (= SYNAPSIS-DEPENDENT GENE EXPRESSION), WHERE TARAPTIC PAIRING OF CHROMOSOMES CARRYING GENES WITH WHICH ZESTE INTERACTS INFLUENCES THE EXPRESSION OF THESE GENES. ZESTE BINDS TO DNA AND STIMULATES TRANSCRIPTION FROM A NEARBY PROMOTER.

TRANSCRIPTION FROM A NEARBY PROMOTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20196011; PubMed-10731137;

Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,

Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadie

Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borko

Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S

Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,

Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,

Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,

McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C
                                                                                                                             EMBL; L13046; AAA29029.1; -
EMBL; L13047; AAA29030.1; -
EMBL; L13048; AAA29031.1; -
EMBL; AE003424; AAF45783.1;
EMBL; AE003424; CAB63525.1;
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EMBL;
EMBL;
EMBL;
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  DOMAIN
DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ME-K1, ME-1 MEDLINE=93360802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Multimerization of the Drosophila zeste protein is required
efficient DNA binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93259149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster.
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melanogaster.":
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                                         FlyBase; FBg
DNA-binding;
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                               NIT_MET
                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content is ified and this statement is not removed. Usage by and fittes requires a license agreement (See http://www.isb-sibsend an email to license@isb-sib.ch).
                                                                                      A26639;
S01272;
S12569;
                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                   Y00049;
X06743;
L13043;
L13044;
L13045;
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                                                        FBgn0004050; z
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Transcription : 0 0 0 0 1 46 47 127
                                                                                   A26639.
S01272.
S12569.
                                                                                                                                                      ; AAA29029.1; -.; AAA29030.1; -.; AAA29031.1; -.
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                                         regulation; Nuclear
HYDROPHOBIC.
SPECIFIC, WITH
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K., Zhu S., Zhu X.,
 ZESTE LOCUS
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                                        protein;
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                                         Polymorphism
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Smith H.O.,
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RESULT 4

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CONFLICT
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium-dependent multivitamin transporter (Na(+)-dependent
                                                                                                                                                                               EMBL; AF116241; AAD37502.1;
EMBL; AF069307; AAD31727.1;
EMBL; AF081571; AAD37481.1;
                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dependent multivitamin transporter.";
Arch. Biochem. Biophys. 366:95-106(1999).
-I- FUNCTION: TRANSPORTS PANTOTHENATE, BIOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang H., Huang W., Fei Y.-J., Xia H., Yang-F
Devoe L.D., Ganapathy V., Prasad P.D.;
"Human placental Na+-dependent multivitamin
functional expression, gene structure, and c
J. Biol. Chem. 274:14875-14883(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
TIGRENAMS; TIGRO0813; SSS; 1.
PROSITE; PS00456; NA_SOLUT_SYMP_1;
PROSITE; PS00457; NA_SOLUT_SYMP_2;
PROSITE; PS50283; NA_SOLUT_SYMP_3;
                                                                                    InterPro; IPR001734; Na/solut_symport.
Pfam; PF00474; SSF; 1.
                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prasad P.D., Wang Ganapathy V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99268779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLC5A6 OR SMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multivitamin transporter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Y289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular and functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99262640;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449
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                                                                                                                                                                                                                                                                                                                                                                                                                         PRESENCE OF SODIUM.

SUBCELLULAR LOCATION: Integral membrane p
SUBCELLULAR LOCATION: THE SODIUM:SOLUTE
SIMILARITY: BELONGS TO THE SODIUM:SOLUTE
                                                                                                                                   604024
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                                                                                                                                                          HGNC:11041;
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496
574 AA;
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152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10329687;
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496
61845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLY-RICH.
GLN/ALA-RICH (OPA-REPEAT INVOLVED IN
GRANSCRIPTIONAL ACTIVATION OR REPRESSI
AT DIFFERENT TARGET LOCI) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN STRAIN ME-K2).
S -> A (IN REF. 4 AND 5).
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                       FALSE_NEG
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E SYMPORTER FAMILY (SSF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intestinal
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                                                                                                                                                                                                                                                                                                                                                               restrictions
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                                                                                                                                                                                                                                                                                                                                                                                    EMBL outstation
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport;
                                                                  DOMAIN
                                                                          NON_TER
                                                                                  Microtubules.
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                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                             TISSUE=Breast
                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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        24
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                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                          European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
                                                                                                                                                                                                           nitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. FUNCTION: Gamma-tubulin complex is necessary for microtublule nucleation at the centrosome (By similarity).
HPVLSFL
                                                                                                                                                                            SIMILARITY: BELONGS
                                                                                                                                                                                    SUBCELLULAR LOCATION:
                                                                                                                                                                                            GCP3, GCP4,
                                                                                                                                                                                                  SUBUNIT: Gamma-tubulin complex is composed of gamma-tubulin, GCP2,
                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                       MOUSE
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                        Similarity 7; Conserv
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                                                                                                                   requires
                                                                                                                                                                                                                                                                              Eutheria;
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677 1
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                       8.9%;
ilarity 100.0%;
Conservative (
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                                                         ΑA;
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                                                                                                                                                                                            GCP5 and GCP6 (By similarity)
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599
78348 ⊁
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                                                                                                                                                                                                                                                                              Rodentia;
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100.0%;
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                                                                                                                                                                                                                                                                                                             component
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                                                                                                                                                                            TO THE GCP FAMILY
                                                          MW.
                                                                                                                                                                                   Centrosome (By similarity).
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                                Score 7; Pred. No
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                         Mismatches
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(GCP-3) (Fragment).
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Query Match
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                                  CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096Cw5; 043631; 060852; 060853; 096179; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 16-JUN-2002 (Rel. 41, Last annotation update) 6amma-tubulin complex component 3 (GCP-3) (Spindle pole body protein
                                                                                                                                         VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tassin A.-M., Celati C., Moudjou M., Borr "Characterization of the human homologue association with gamma-tubulin.";
                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              produced by alternative splicing.
-1- TISSUE SPECIFICITY: Ubiquitously expre-
-1- SIMILARITY: BELONGS TO THE GCP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AN MEDLINE=98234404; PubMed=9566969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1). TISSUE=Cervical carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institumodified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleation at the centrosome.
-1- SUBUNIT: Gamma-tubulin complex is composed GCP3, GCP4, GCP5 and GCP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBar -!- FUNCTION: Gamma-tubulin complex is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Eye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spindle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spc98 homolog) (hSpc98) (hGCP3) (h104p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCP3_HUMAN
                                                                                                                                                                                                Microtubules;
DOMAIN 8:
                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                                            entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Centrosome.
-1- ALTERNATIVE PRODUCTS: 3 isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy S.M., Urbani L.,
"The mammalian gamma-tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98234402; PubMed=9566967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                        VARSPLIC
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AJ003062;
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BC007763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mmalian gamma-tubulin complex pole body components spc97p a Biol. 141:663-674(1998).
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                                                                                                                                                                                                                                                                                                                                                          requires a license agreement
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RWI -> PTRVFFTHVFFTRDFFTRDFPHHVFFTRVFFTRV
WHSLCFRTRL (IN ISOFORM 3).
MISSING (IN ISOFORM 3).
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                       Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
conormatophyta; Coniferopsida; Coniferales; Pinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Spermatophyta; Magnoliophyta; Panicoideae; Andropogoneae; Zo NCBI_TaxID-4577;
                                                                                                             MFS14 protein MFS14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Loss of all ndh genes as determined by sequencing the echloroplast genome of the black pine Pinus thunbergii."; Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE REACTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPEP
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Pfam; PF02533; PsbK; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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NCBI_TaxID=3350;
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56 AA;
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zuki J., Ito S.,
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Pred. No
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01-NOV-1990
                                                                                                                                                                                                       MEDLINE=90111716; PubMed=2607341; Storey C.C., Lusher M., Richmond S.J.; a phage which "Analysis of the complete nucleotide sequence of Chpl, a phage which infects avian Chlamydia psittaci."; J. Gen. Virol. 70:3381-3390(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
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STRAIN-CV. BE10; TISSUE-Tassel;

MEDLINE-94004987; PubMed-8401606;

Wright S.Y., Suner M.-M., Bell P.J., Vaudin M., Greenland A.J.;

"Isolation and characterization of male flower cDNAs from maize."

Plant J. 3:41-49(1993)

-1- TISSUE SPECIFICITY: ENHANCED EXPRESSION IN MALE FLOWERS.

ACCUMULATES IN THE TAPETUM.
                                                                       PIR;
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                     Bacteriophage Chp1.
Viruses; ssDNA viruses;
                                                                                                                                                                                                                                                                                                                             Protein VP3 (ORF3).
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                                                          Structural
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 Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69183;
                                               protein.
145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AA;
                                                                                                                                                                                                                                                                                                                                                     (Rel.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                       JU0347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S25104.
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                       16,
16,
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126
12653
                                                                                                                                                                                                                                                                   AND PARTIAL
                                                16681 MW;
                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                       7.68;
                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.68;
                                                                                                                                                                                                                                                                                                    Microviridae; Microvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 1; Pred. No. 32; 0; Mismatches
            Score 6;
Pred. No
                                                                                                                                is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR 24, OR 26 (POTENTIAL).
MFS14 PROTEIN.
; 67F2813AFF8C55E5 CRC64;
                                                6B4DFA64663587CD
                                                                                                                                                                                                                                                                   SEQUENCE
             No.
                                                                                                                                                                                                                                                                                                                                                                                         145
                                                                                                                                                                                                                                                                                                                                        update)
                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no
                                                                                                                                                          There are no
                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                            as its content
                                                                                                                    http://www.isb-sib
                                                                                                                                  Usage
                       Length 145;
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Matches

0

Mismatches

0

Indels

0,

Gaps

S

39

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LMBV_CHICK
LMBV_CHICK
ID LMBV_C
AC Q01636
DT 01-NOV
DT 01-NOV
DT 15-JUN
DE Lamini
OS Gallus
OC Eukary
OC Archos
OC Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
GSPJ_E
GSPJ_E
AC P45761
DT 01-NOV
DT 16-OCT
CC Escher
OC Escher
OC Escher
OC ATRAIN
RX MEDIATI
RA Blattn
RA MAU B.
RT THE C
RL Scienc
CC -!- FU
CC -!- FU
CC -!- FU
CC -!- FU
CC This S
CC This S
CC This S
CC Use E
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CC CHALL
DR EMBL;
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DR EMBL;
DR EMBL;
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ET PROPEI
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Best Local :
                                                                                           01-NOV-1997
01-NOV-1997
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSPJ_ECOLI
P45761;
01-NOV-1995
                                                                                                                                                       LMBV_CHICK
Q01636;
                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR EXPORT OF PROTEINS (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE PULJ/OUTJ/XPSJ/EXEJ/XCPW FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., 1 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Mau B., Shao Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                       Archosauria;
                                         Eukaryota; Metazoa;
                                                           Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001120; Prok_N_methyltn.
PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000409; AAC76356.1; -. EcoGene; EG12893; gspJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSPJ OR B3331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 16-OCT-2001 (Rel.
                                                                               Laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable
                                                                                                                                                                                                                                                                                              44 PLAPLS
                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFYSLP
                                                                                                                                                                                                                                                                          PLAPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U18997; AAA58128.1;
                                                                         1997 (Rel. 35, Created)
1997 (Rel. 35, Last sequence up
2002 (Rel. 41, Last annotation
beta-1 chain variant (Laminin
                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPRO01120; Propson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              001 (Rel. 40, Last general secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methylation; Complete proteome.

1 7 BY SIMILARITY
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(Rel. 32, Last seq
(Rel. 40, Last ann
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                                                                                                                                                                                                                                                                                                                                                    Conservative
                       Aves;
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                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                   Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
                                   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                             8
22231
                                                                                                                                                                                                                                                                                                                                                                  7.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                  Score 6; DB 1; Pred. No. 47; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             METHYLATION (BY SIMILARITY).
4A25DB082106B1C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBABLE GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN J
                     Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ion update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                   update:
                                                                           update)
beta-1-2
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                                                                                                                                                                           198
                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rode C.K., May
                   Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECRETION PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY (GSP) FOR THE
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                        Length 195
                                                                           chain) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .K., Mayhew
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burland V., hew G.F.,
                                                                                                                                                                                                                                                                                                                                                  <u>.</u>.
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AC OCC OCC RANGE R
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                     01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem.
"LAF-4 encodes a lymphoid nuclear protein with transactivation potential that is homologous to AF-4, the gene fused to MLL in t(4;11) leukemias.";
                                                        MEDLINE-96141096;
Ma C., Staudt L.M.
                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                 LAF-4 protein
                                                                                                                                                                                                                                                                                                               P51827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE: PS01248; LAMININ_TYPE_EGF;
Extracellular matrix; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001886; LamNT.
InterPro; IPR002049; Laminin_EGF
Pfam; PF00055; laminin_Nterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L00963; AAA49140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93015947; PubMed=1400373;
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                                                                                                                                                                                                                                                                                                                                   LAF4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aminin
                                                                                                                                                                                                                                                                                                                                                                                                                                   59 PRPAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 PRPAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with other extracellular matrix components, SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, betta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3101. Chem. 267:20555-20557(1992).

FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPONENT )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comprising one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD002082; LamNT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
198 AA;
                                                                                                                                                                                                                               (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
in (Lymphoid nuclear protein related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LamNT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
>198
198
21830 <sub>1</sub>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B1 chain variant
                                                                              PubMed~8555498;
                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               long and three short arms with globules at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAMININ N-TERMINAL (DOMAIN
                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6FD669761892C442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in avian eye.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL.
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                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
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Quirk P.G., Hicks D.B., Krulwich T.A.;
"Cloning of the cta operon from alkaliphilic Bacillus firmus
characterization of the pH-regulated cytochrome caa3 oxidase
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PROSITE; PS50253; COX3; 1.
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-i- FUNCTION: PUTATIVE TRANSCRIPTION ACTIVATOR THAT MAY FUNCTION
              PROSITE;
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                                                                                                                                                                              send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
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Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Rzevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.
                                                                                                      Winters P., Wipat A., Yoshida K., Yoshida K.,
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                    Nature 390:249-256(1997).
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H.F., Zumstein E., Yoshikawa
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STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Posfai G., Hackett J., Klink S., Boutin A., Potamousis K.,

Posfai G., Hackett J., Lin A., Dimalanta E.T., Potamousis K.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Grotbeck E.J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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InterPro; IPR003669; Polysac_CapD.
Pfam; PF02719; Polysacc_synt_2; 1.
Hypothetical protein; Complete pro
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     MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., J
Iida T., Takami H., Honda T., Sasakawa C., Ogasa
                                                         SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD
                                                                                                                                                                                                                                                                                         Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., Rk Gregor J., Davis N.W., Kirkpatrick H.A., Go
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01-OCT-1996 (Rel. 34, Last
16-OCT-2001 (Rel. 40, Last
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                                                                                               sequence of enterohaemorrhagic 409:529-533(2001).
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Ogasawara
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Dunn C.A., O'Handley S.F., Frick D.N., Bessman M.J.;
"Studies on the Aup-ribose pyrophosphatase subfamily
hydrolases and tentative identification of trgB, a g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia 0157:H7 and genomic comparison with a laboratory strain K-1 DNA Res. 8:11-22(2001).
                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate.
-!- COFACTOR: REQUIRES DIVALENT IONS: MAGNESIUM, MANGANESE OR ZINC.
-!- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. NUDF SUBFAMILY.
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J. Biol. Chem. 274:32318-32324(1999).
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Copyright (c) 1993 - 2003 Compugen
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B88561
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215	214	209	209	209	209	207	206	205	205	198	195	191	182	182	171
N	N	N	N	N	N	N	N	2	N	N	N	N	N	N	2
S78307	T29080	T21742	н65090	в91119	A85964	A69941	E45335	C90665	F85515	A45067	F65126	T04853	F69221	S76346	T43959
plastoquinol-plas	probable transcrip	hypothetical prote	ADPribose diphosp	ADPribose diphosp	ADPribose diphospl	capsular polysacch	cytochrome-c oxida	hypothetical prote	unknown protein en	laminin B1 chain v	probable general s	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote

ALIGNMENTS

A;Reference number: AB180
A;Accession: AH1848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <KUR>
A;Cross-references: GB:B# C; Genetics: A; Introns: 6 C; Keywords: n, cross-references: GB:BA000019; PIDN:BAB72295.1; PID:g17129682; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: Ab1807; MUID:21595285; PMID:11759840 hypothetical protein all0337 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AH1848 submitted to the EMBL Data Library, February 1992
A;Reference number: S40973
A;Accession: S40979
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-292 <BER> RESULT 2
\$40979
hypothetical protein F58A4.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Feb-1997
C;Accession: \$40979
R;Berks, M. Q RESULT AH1848 밁 A; Gene: all0337 A; Cross-references: EMBL: Z22179 Query Match Best Local S Matches 7 Query Match Best Local Matches 56 25 PVLSFLR 31 PVLSFLR 62 60/2; 133/1; nucleus Similarity 7; Conserv Similarity Conservative Conservative 273/1 8.9%; >cc 100.0%; Pr 8.9%; b; Score 7; DB 2
b; Pred. No. 12;
0; Mismatches 0; Score 7; [Mismatches DB 1 . DB . ω Ν Length 121; 0; Length 292 Indels Indels 0 0 Gaps Gaps 7120 0 0

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RESULT 5
AH2797
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A97577
hypothetical protein AGR_C_3311 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: A97577
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthmer, ; Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <STO
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C;Speciles: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: B88561
                                                                                 conserved hypothetical protein Atul800 [imported] - Agrobacterium tumefaciehs C; Species: Agrobacterium tumefaciens
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A;Molecule type: DNA
A;Residues: 1-389 <KUR>
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A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; anonymous, The C. election Science 282, 2012-2018,
                                                                                                                                                                                                                                                                                                                   A; Map
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Pred. No.
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Doughty, D.; Scott, C.; Lappas, C.;
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                  Kutyavin,
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                                Wood, G.E.; Chen, Y.; Woo,
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           Local Similarity hes 7; Conserv
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R;Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Chem. Biol. 3, 155-162, 1998
A;Title: Sequencing and analysis of genes involved in the biosynt A;Fefrence number: Z18804
                                                                                                                                                                                C; Species: Amycolatopsis orientalis C; Date: 02-Sep-2000 #sequence_revision C; Accession: T17478
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Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A70300; M
A;Accession: B70473
A;Status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: B70473
R;Deckert, G.; Warren, P.V.;
                                                A;Cross-references: EMBL:AJ223998; NID:e1251208; PID:e1251217;
                                                                A; Molecule type: DNA
A; Residues: 1-495 <V
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A; Title: The complete gen
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                                                                                          A; Status: preliminary; translated
                                                                                                                                                                                                                             hypothetical protein PCZA361.11 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE008688; PIDN:AAL42798.1; A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-389 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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Best Local
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| 428 VLSFLRP 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-436 <AQF>
                                                                  1-495 <VAN>
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                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE000768; NID:g2984249; PIDN:AAC07778.1;
ce: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001
, Y.; Biddle,
                                                                                                                                                                                                                                                                                                                                                                       8.9%;
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                      8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e of the hyperthermophilic bacterium MUID:98196666; PMID:9537320
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Pred. No.
                      Score 7;
                                                                                          from
                                                                                                                                                                                                                        Amycolatopsis orientalis
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Pred. No.
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                                                                                           GB/EMBL/DDBJ
                                                                                                                                                                                             02-Sep-2000
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DB 19;
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17;
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15;
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                     2;
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                     Length 495;
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                                                                                                                                    biosynthesis of a vancomyci
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                                                 PIDN:CAA11769.1
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                                                                                                                                                                  Kershaw,
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RESULT 10
S01272
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EMBO J. 6, 791-799, 1987
A;Title: Structure and sequence of the Dros
A;Reference number: A26639; MUID:87218538;
A;Accession: A26639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A70300; MUID:98198666; PMID:9537320 A;Accession: C70311
                                 R; Mansukhani, A.; Gunaratne, P.H.; Mol. Gen. Genet. 211, 121-128, 1988
                                                                 regulatory protein zeste - fruit fly (Drosophila melanogaster) (;Species: Drosophila melanogaster C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change C;Accession: S01272
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                                                                                                                                                                                                                                                                                                                                      A;Cross-references: FlyBase:FBgn0004050
A;Introns: 103/2; 284/1
C;Keywords: DNA binding; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-555 <PIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory protein zeste - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Feb-1997
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A26639
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C;Superfamily: Aquifex aeolicus hypothetical protein ag_116
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C70311
                 Mol. Gen. Genet. 211, 121-128, 19
A;Title: Nucleotide sequence and
                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: zeste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
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Best Local
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                        transcription regulation
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e and structural MUID:88142560; E
                                                 P.H.; Sherwood, P.W.; Sneath, B.J.; Goldberg, M.L.
                                                                                                                                                                                                                                                                                       Score 7;
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538; PMID:3582372
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 l analysis of PMID:3125410
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5. 21;
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                   the zeste locus of Drosophila
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RESULT 11
T15862
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                                                                                                                                                                                                                                             hypothetical protein AT4902510 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-20 C;Accession: A85032 C;Accession: A85032 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, Nature 402, 769-777, 1999
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A85032
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A;Cross-references: FlyBase:FBgn0004050
A;Introns: 123/2; 304/1
C;Keywords: DNA binding; transcription:
                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-865 <STO>
                                                                                                                                                                                          A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198 A;Accession: A85032
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V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1999 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-574 <MAN>
A;Cross-references: EMBL:X06743; NID:g8852; PIDN:CAA29918.1; PID:g8853
A;Note: the authors translated the codon CGT for residue 366 as Ala
C;Genetics:
                                                                      A; Map
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                                                                                          A;Gene: AT4g02510
                                                                                                                         A; Cross-references: GB: NC_001268; NID: g7269011; PIDN: CAB80744.1;
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                     Best
                                    Query Match
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Best Local
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Best Local
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nes 7; Conserv
                     Local
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   Similarity 7; Conserv
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   Conservative
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100.0%;
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                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293/3;
                                  Length 865;
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A, Experimental Source: cultivar Columbia R; Kalicki, J.; Elliott, G.; Cloud, J. submitted to the EMBL Data Library, May 1998 A, Description: The sequence of A. thaliana Tl A; Reference number: Z14290 A, Accession: T01299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: chloroplast import-associated protein, GTP-binding; protein Ti4p8.2: C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12:Feb-1999 #sequence_revision 12:Feb-1999 #text_change 02:Feb-2001
C;Accession: T01098; T01299
C;Accession: T01098; T0129
C;Accession: N; Johnson, D; Schutz, K; Gnoj, L; Hoffman, J; Till, S; de la Bastide, R; Kaplan, N; Johnson, D; Schutz, K; Gnoj, R; McCombie, W.R.
hi, Martienssen, R; Chen, E::, Wilson, R; McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-372,'EQQ',376-879 <KES>
A;Cross references: GB:L36857; NID:g576508; PIDN:AAA53276.1; PID:g576509
C;Keywords: chloroplast; GTP binding; membrane protein; nucleotide binding;
F;245-252/Region: nucleotide-binding motif A (P-loop)
A;Molecule type: DNA
A;Residues: 1-1503 <KAL>
A;Residues: 1-1503 <KAL>
A;Cross-references: EMBL.AF069298; NID:g3193282; PID:g3193301
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1998
A;Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
A;Reference number: Z14248
A;Accession: T01098
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                                                                                                                     A; Status: translated from GB/EMBL/DDBJ
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A; Cross-references: EMBL: AC002330; NID: g2262135; PID: g3892053
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-1503 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chloroplast outer envelope protein OEP86 homolog T10P11.19 - arabidopsis thaliana N.Alternate names: chloroplast import-associated protein, GTP-binding; protein T1.
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A;Accession: A55171
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chloroplast outer envelope protein OEP86 precursor - garden pea N;Alternate names: chloroplast import-associated protein IAP86,
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A; Molecule type: mRNA
A: Residues: 1-137,'Q',139-875,877-879 <HI2>
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A; Residues: 1-87
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Best Local Similarity
watches 7; Conserv
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C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology F;24-435/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology
Search completed: January 14, 2003, 17:14:59 Job time: 7.6004 secs
                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable multi-domain beta keto-acyl synthase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
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C;Keywords: chloroplast; GTP binding; membrane protein; nucleotide binding; P-loop
F;862-869/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL109747; PIDN:CAB52354.1; GSPDB:GN00070; A;Experimental source: strain A3(2)
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A; Residues: 1-2240 <SEE>
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A;Accession: T37057
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100.0%; Pred. No.
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Library, August 1999
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                                                                                                                                                           Score 7; Pred. No
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                                                                                                                                         Mismatches
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o. 53;
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5. 76;
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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                  Score
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79
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(without alignments)
1036.856 Million cell updates/sec
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Human HER2 intron
Human p68HER-2 ECD
Human p68HER-2 gen
Human p68HER-2 Human p68HER-2
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Human p68HER-2 ECD
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Human p68HER-2 ECD Human HER2 intron Human p68HER-2 par HER2 protein conta Human brain expres Human bone marrow	p68HER-2 p68HER-2 p68HER-2 C-termina p68HER-2 p68HER-2 p68HER-2 p68HER-2 p68HER-2 p68HER-2 p68HER-2 p68HER-2 p68HER-2 p68HER-2 p68HER-2	Truncated HER-2, p Human p68HER-2 gen

ALIGNMENTS

AAY97239 standard; protein; 79

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04-DEC-2000 (first entry)

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Misc-difference

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HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa.
                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herceptin (RTM) (a marketed humanized monoclonal antibody that is used for the treatment of cancer and binds to the ECD of HER-2). The methods, compositions, polypeptides and antibodies are used to treat solid tumours such as breast cancer, small cell lung carcinoma, ovarian cancer and/or colon cancer, especially where over-expression of HER-2 is
                                                                                        15-NOV-2001
                                                                                                                         AAE09180;
                                                                                                                                                   AAE09180 standard;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the receptor-like tyrosine kinase HER-2 to treat solid tumors
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                                                           p68HER-2
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                                                        ECDIIIa generic sequence
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p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 ECDIIIa
                                                                                particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10'8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of
Sequence
                                                                                                                                                                            Claim 1; Page 52-53; 61pp; English.
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                    generic sequence.
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Query Match

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 WPI; 2002-269185/31
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; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The method involves administering an agent that binds to an extracelly domain (ECD) of EGFR. The invention also relates to a naturally occurr inhibitor of HER-2 receptor tyrosine kinase called herstatin. The coexpression of herstatin with p185HER2 causes a striking reduction in c growth that corresponds with suppression of p185 autophosphorylation. method or a pharmaceutical composition is useful for treating a solid tumour (selected from squamous cell carcinoma, lung carcinoma, colon carcinoma and glial cell tumour) characterised by EGFR expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating solid tumor characterized by expression of endothelial growth factor receptor, involves administering recombinant herstatin that binds to extracellular domain of the endothelial growth factor recepto:
 Misc-difference
                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                               HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa.
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                                                Misc-difference
                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human p68HER-2 ECDIIIa generic sequence #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a method for treating a solid characterised by endothelial growth factor receptor (EGFR) exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is a protein encoded by human HER2 intron 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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/note= "Encoded
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RESULT 5
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Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p80HER-2 which lacks the transmembrane and intracellular domains of the product of the control of the contr
                                                                                                                                                                                                                                                                                                nucleic acids encoding these are useful to treat, diagnose and solid tumours. The present sequence is human p68HFR-2 properties generic sequence
  Human
                              15-NOV-2001
                                                                                    AAE09181 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide, which binds to the extracellular domain of HER-2 the treatment of hard tumors - \,
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                                                                                                                                                                                                                                                                                                                                            185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. he ECDIIIA-containing polypeptides bind tightly to, and thus antagonise he HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
                                                                                                                                                           2001-529934/58
  p68HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page 57;
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                        79
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                                                                                                                                                                                                                  Conservative
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  generic sequence #1.
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 The invention relates to novel HER-2 (herstatin-2) antagonist
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HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa.
Claim 8; Page 53-54; 61pp; English.
                                                              WPI; 2001-529934/58.
N-PSDB; AAD15844.
                                                                                                 Clinton G,
                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                         New polypeptide, which binds to
the treatment of hard tumors -
                                                                                                                         (UYOR-) UNIV OREGON HEALTH SCI.
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the specification"
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify
                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P68HER-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE09208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE09208 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       solid tumours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p68HER-2 generic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECDIIIa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; polymorphism; cytostatic; gene therapy;
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/note- "Extracellular do
124
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341..419
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in the specification"
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Represented as specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identical to N-terminal region of p185HER-2"
                                        Unknown
                                                                                                                                    Unknown
                                                                                                                                                                             Asp, Ala,
                                                                                                                                                                                                                                                                                                                      Unknown
                                                                                                                                                                                                                                                                                                                                                                   Unknown
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parent sequence shown
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                                                                                                                                                                                                   the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identification tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.
                                                                                                                                                                                                                                                                of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
                                                                                                                                                       derived from p68HER-2 generic sequence sequence listing (AAE09181).
                                                                                                                           Sequence
                                                                                                                                                                         Note: The present sequence is derived from p68HER-2 generic
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel HER-2 (herstatin-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYOR-)
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341 GXHSXXPRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL
                                                                          Local
             1 GXHSXXPRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, which binds
treatment of hard tumors
                                                            Similarity
48; Conserv
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                                                                                                                           419 AA;
                                                           51.9%;
ilarity 100.0%;
Conservative
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                                                            <u>,</u>
                                                           Score 41; DB
Pred. No. 1.5
0; Mismatches
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                                                                                                                                                                                        not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extracellular domain of HER-2 for
                                                                                                                                                                         (SEQ
                                                                           DB 22
                                                                                                                                                                       in the specification but is (SEQ ID NO:2) shown in the
                                                                                            22;
                                                                                          Length 419
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                              antagonist
                                                                                                                                                                                                                                      and identify
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RESULT 7
AAE09210
ID AAE0
 Key
Region
                                                                                                        HER-2; herstatin;
solid tumour; can
                                                                                                                                                                  AAE09210;
                                                                                                                                                                                   AAE09210 standard; Protein;
          Misc-difference
                                    Domain
                                                                              Homo sapiens
                                                                                               p68HER-2; ECDIIIa;
                                                                                                                                 Human p68HER-2 generic protein
                                                                                                                                                   15-NOV-2001
                                                                                                                                                 (first entry)
                                                                                                        cancer;
        /iabel= ECDIIIa_variant
/note= "Extracellular dd
124
                                   /note= "I
341..419
 /note=
                                                            Location/Qualifiers
                                                                                                                antagonist;
                                                                                                variant.
                                                                                                       polymorphism;
"Represented as Agn
                                           "Identical to N-terminal region
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                                                                                                                extracellular domain;
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                                                                                                       cytostatic;
                   domain IIIa
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the parent sequence shown
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                  variant"
                                                                                                                ECD; Herceptin;
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                                           of p185HER-2"
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                                                       Query Match
Best Local (
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                                                                                                                          Note: The derived
                                                                                                                                              p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind trightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.
                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                   Clinton
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                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                      Example 11; Page -;
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                                                                                                                                                                                                                                                                                                                                          polypeptide, which binds to treatment of hard tumors -
2001-529934/58
                                                                                                                        The present sequence is not shown in the specification but is ed from p68HER-2 generic sequence (SEQ ID NO:2) shown in the
                                             18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                           listing
                                                                                         419
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                                             Conservative
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376
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346
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358
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356
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125
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345
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342
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                                                                                                              HER-2 generic sequence (SEQ (AAE09181).
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                                         51.9%; bu
100.0%; Pr
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                      English.
                                                       Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                      the
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 generic sequence (AAE09181)
Arg"
                                                        No.
                                                                                                                                                                                                                                                                                                                                                      extracellular domain of HER-2
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                                                       DB 22;
                                                       .5e-35;
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                                                                Length 419;
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ARESULT 8
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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular do of HER-2 at a site that is different from the binding site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HER-2; herstatin; antagonist; extracellular domain;
solid tumour; cancer; polymorphism; cytostatic; gene
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE09211 standard; Protein; 419
                                                                                Example 11; Page -; 61pp; English.
                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                               Clinton
                                                                                                                                                                                                                                                                   (UYOR-) UNIV OREGON HEALTH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE09211
                                                                                                                        polypeptide, which binds to the treatment of hard tumors -
                                                                                                                                                                                     2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P68HER-2
                                                                                                                                                                                                                             ڻ
ص
                                                                                                                                                                                                                             Henner WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                           2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             generic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "p68HER-2
substituted with
413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Identical to N-terminal region of pl85HER-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Represented as
in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label- Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                             Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                generic sequence (AAE09181)
Leu"
                                                                                                                                             extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               و
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECD;
                                                                                                                                           of HER-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herceptin;
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domain

humanised (ECD)

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RESULT 9
AAE09212
ID AAE0
XX AAE0
XX AAE0
XX Huma
AX HER-
AX HOMC
XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody, Herceptin, at an affinity of at least 10^8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The present sequence is not shown derived from p68HER-2 generic sequence sequence listing (AAE09181).
                                                                                                                                           Misc-difference
                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-2; herstatin;
solid tumour; can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human p68HER-2 generic protein variant 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE09212 standard; Protein; 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein
    Misc-difference
                                                                                                Misc-difference
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE09212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing ECDIIIa variant sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 51.9%; S
Similarity 100.0%;
48; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341..419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= ECDIIIa_variant
/note= "Extracellular d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Identical to N-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Represented as
in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                           'label= Unknown
                           label-
                                                                        label- Unknown
                                                                                                                                                                                                                                                                                                               label- Unknown
                                                                                                                                                                                                                                                                                                                                                              label= Unknown
                                                                                                                                                                    label=
                                                                                                                                                                                                                   label=
                                                                                                                                                                                                                                                                  label=
                                                                                                                    label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the "Represented as
the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agonist; extracellular domain;
polymorphism; cytostatic; gen
                           Unknown
                                                                                                                       Unknown
                                                                                                                                                                    Unknown
                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B; Score 41; DB; Pred. No. 1.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not shown in the specification but is sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; I
1.5e-35;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the parent sequence shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parent sequence shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herceptin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p185HER-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the alternative transcript is a truncated HER-2 protein designated p68HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10<sup>8</sup>. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product
                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The present sequence is not shown derived from p68HER-2 generic sequence sequence listing (AAE09181).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page -; 61pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-2000;
                                                                                                                                           Human;
                                                                                                                                                                     Human
                                                                                                                                                                                              18-JUN-2002
                                                                                                                                                                                                                        AAE20348;
                                                                                                                                                                                                                                                 AAE20348 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-2001; 2001WO-US05327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200161356-A1
                                              Misc-difference
                                                                                                                             herstatin;
                                                                                                                                                                                                                                                                                                                  341
                                                                                                                                                                                                                                                                                                               polypeptide, which binds to the treatment of hard tumors -
                                                                                      sapiens.
                                                                                                                                                                    truncated
                                                                                                              tumour; endothelial growth factor receptor; EGFR;
itin; HER-2 receptor tyrosine kinase; squamous cell
glial cell tumour; cell growth.
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Henner WD,
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to novel HER-2 (herstatin-2)
                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
                                                Location/Qualifiers 342
                                                                                                                                                                    HER2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "p68HER-2 generic sequence (AAE09181) Xaa
substituted with Asn"
                                  'label= Thr,
           'label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                  419
                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Þ
                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extracellular domain of HER-2 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification but is NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                                              Length 419
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antagonist
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 11
AAY97240
   E K X D X D X X X X I D
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                                                                                                                                                       Matches
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                              The present invention relates to a method for treating a solid tumour characterised by endothelial growth factor receptor (EGFR) expression. The method involves administering an agent that binds to an extracellular domain (ECD) of EGFR. The invention also relates to a naturally occurring inhibitor of HER-2 receptor tyrosine kinase called herstatin. The co-
  HER-2; erbB-2; oncoge extracellular domain
                          Truncated HER-2, p68-HER-2.
                                           04-DEC-2000
                                                            AAY97240;
                                                                            AAY97240 standard; protein;
                                                                                                                                                                                                             tumour (selected from squamous cell carcinoma, lung carcinoma, colon carcinoma and glial cell tumour) characterised by EGFR expression. The present sequence is human truncated HER2 protein that lacks transmembrane
                                                                                                                                                                                                                                     expression of herstatin with p185HER2 causes a striking reduction in growth that corresponds with suppression of p185 autophosphorylation method or a pharmaceutical composition is useful for treating a solid
                                                                                                                                                                                                                                                                                                                                       Treating solid tumor characterized by expression of endothelial growth factor receptor, involves administering recombinant herstatin that binds to extracellular domain of the endothelial growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                           Clinton
                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2001;
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                                                                                                                      341
                                                                                                                                                               Local
                                                                                                                             1 GXHSXXPRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 48
                                                                                                                                                                                                       intracellular domains.
                                                                                                                     GXHSXXPRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 388
                                                                                                                                                                                                                                                                                                                 1; Page 78-80;
                                                                                                                                                              Similarity
                                                                                                                                                                                       419 AA;
                                                                                                                                                      Conservative
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US25502
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          oncogene;
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356
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 receptor-like tyrosine kinase; inso
a; antagonist; intron 8; C-terminal
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                                                                                                                                                     0;
                                                                                                                                                              Score 41;
Pred. No.
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                                                                                                                                                           DB 23; 1
                                                                                                                                                                     Length 419;
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                 Query Match
                 Sequence
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p185-HER-2 without activating HER-2. It could therefore block dimerization of p185-HER-2. The p68HER-2 polypeptide binds to a sittle ECD of HER-2 that is different from the site of binding for Herceptin (RTM) (a marketed humanized monoclonal antibody that is for the treatment of cancer and binds to the ECD of HER-2). The me
                                                                                                                                                                                            HER-2 mRNA of 4.8 kb with a 274 bp insert (intron 8) has been identified. The retained intron is in-frame and encodes a 79 amino acid extension designated ECDIIIa (the present sequence), which is inserted a residue 340 of pl85-HER-2. The alternative mRNA predicts a truncated HER-2 protein (approximately 68 kDa) that lacks the transmembrane and intracellular domains (see AAY97240). p88HER-2 specifically binds to
                                                                                                                                                                                                                                                                                                                                carcinoma cells in culture and is found in serum of some cancer patients and may be a serum marker of metastatic breast cancer. An alternative HER-2 mRNA of 4.8 kb with a 274 bp insert /internative
compositions, polypeptides and antibodies are used to treat solid tumours such as breast cancer, small cell lung carcinoma, ovarian and/or colon cancer, especially where over-expression of HER-2 is
                                                                                                                                                                                                                                                                                                                                                                                                      HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. extracellular domain of p185-HER-2 is proteolytically shed from breas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 39-40; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast, lung, ovaries and colon
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                                                                                                                                                           IER-2 protein (apparametrically), p68HER-2 specifically intracellular domains (see AAY97240), p68HER-2 specifically intracellular domains (see AAY97240).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides and antibodies that bind to the extracellular e receptor-like tyrosine kinase HER-2 to treat solid tumors
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New polypeptide, which binds to the extracellular domain of HER-2
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solld tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human p68HER-2
                                               Clinton
                                                                                            16-FEB-2000; 2000US-0506079
                                                                                                                  16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GXHSXXPRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Conservative 0;
                                              Ġ
                                                                      UNIV OREGON HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECDIIIa; variant.
                                              Henner WD,
                                                                                                                  2001WO-US05327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    generic
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in the specification"
                                                                                                                                                                                         /label= Unknown
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in the specification"
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                                                                                                                                                                                                             'label= Unknown
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'note- "Extracellular d
                                                                                                                                                                                                                                                             label- Unknown
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10%. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.
                                             Misc-difference
                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Human p68HER-2 generic protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the alternative transcript is a truncated HER-2 protein design p68HER-2 which lacks the transmembrane and intracellular domains
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                                                                                                                                                                                                                                      Doma in
                                                                                                                                                                                                                                                                                                                    solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p60HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                  HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   AAE09204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa.
The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the treatment of hard tumors
                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 HSXXPRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSXXPRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 100
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 AA;
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
361
                                                                    substituted with
                                                                                                                                                                 125
                                                                                                                                                                                                    124
                                                                                                                                                                                                                                      /note=
                                               356
                                                                                                                                                                            in
                                                                                                                                                                                                             /label= ECDIIIa_variant
/note= "Extracellular d
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                         /note= "Represented as
in the specification"
            label- Unknown
                                                                                            note= "p68HER-2
                                 abel=
                                                         .abel=
                                                                                                                 abel=
                                                                                                                                        the
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100.0%; pr
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                                                                                                                                       "Represented as specification"
                                                                                                                                                                                                                                               "Identical to N-terminal region of p185HER-2"
                                  Unknown
                                                         Unknown
                                                                                                                 Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                        419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB Pred. No. 1.8 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not shown in the specification but is sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                                   variant
                                                                               generic
Pro"
                                                                                                                                                                                                              domain IIIa variant'
                                                                                                                                                  Agn
                                                                                                                                                                                    Agn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
1.8e-34;
                                                                                         sequence (AAE09181)
                                                                                                                                                                                       'n
                                                                                                                                                  in
                                                                                                                                                   the
                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 419
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                                                                                                                                                                                    parent sequence
                                                                                                                                                  parent sequence shown
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cc particularly a polypeptide that binds to the extracellular domain (ECD) cc of HER-2 at a site that is different from the binding site of humanised cc antibody, Herceptin, at an affinity of at least 10°8. The present cc invention is based upon the initial discovery of an alternative HER-2 cc mRNA transcript with 274 bp insert of intron 8. The translation product cf the alternative transcript is a truncated HER-2 protein designated cc p68HER-2 which lacks the transmembrane and intracellular domains of cc p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIa. Cc The ECDIIIA-containing polypeptides bind tightly to, and the us antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the cc nucleic acids encoding these are useful to treat, diagnose and identify containing ECDIIIa variant sequence is human p68HER-2 generic protein cc derived from p68HER-2 generic sequence.
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                                                                                                                                                                     AAE09205
                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                             Matches
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Best Local (
                                      HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
solid tumour; cancer; polymorphism; cytostatic; gene therapy;
                                                                         Human p68HER-2 generic protein variant 3.
                                                                                                       15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
Homo sapiens
                         p68HER-2; ECDIIIa;
                                                                                                                                AAE09205;
                                                                                                                                                         AAE09205 standard;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide, which binds to the extracellular domain of HER-2 for the treatment of hard tumors - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clinton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                    sequence listing (AAE09181).
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                                                                                                                                                                                                                          347
                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                         PRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 388
                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                         48.1%; ilarity 100.0%; Conservative
                                                                                                     (first
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                                    cancer; polymorphism;
                                                                                                                                                                                                                                                                                                                              ΑA;
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376
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                         variant.
                                                                                                                                                         Protein;
                                                                                                     entry)
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                                                                                                                                                                                                                                                                                        Score 38;
Pred. No.
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                                                                                                                                                                                                                                                                            Mismatches
                                    cytostatic;
                                                                                                                                                                                                                                                                                       DB 22; 1
2.4e-32;
                                                                                                                                                                                                                                                                                                 Length 419;
                                    gene
                                                                                                                                                                                                                                                                          Indels
                                    therapy;
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The invention relates to novel HER-2 (herstatin-2) antagonist particularly a polypeptide that binds to the extracellular domain (ECD) of HER-2 at a site that is different from the binding site of humanised antibody, Herceptin, at an affinity of at least 10°8. The present invention is based upon the initial discovery of an alternative HER-2 mRNA transcript with 274 bp insert of intron 8. The translation product of the alternative transcript is a truncated HER-2 protein designated p8HER-2 which lacks the transmembrane and intracellular domains of p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIa. The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the nucleic acids encoding these are useful to treat, diagnose and identify solid tumours. The present sequence is human p68HER-2 generic protein containing ECDIIIa variant sequence.
                       Note: The present sequence is derived from p68HER-2 generic sequence listing (AAE09181).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Region
                                                                                                                                                                                                                                                               Example 11;
                                                                                                                                                                                                                                                                                                                                WPI; 2001-529934/58
                                                                                                                                                                                                                                                                                                                                                                                    (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2000; 2000US-0506079
                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2001; 2001WO-US05327
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                                                                                                                                                                                                                                                                                        polypeptide, which binds to the extracellular domain of \ensuremath{\mathsf{HER-2}} treatment of hard tumors -
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                                                                                                                                                                                                                                                              Page -; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                          Henner WD,
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61
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in the specification"
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                                    not shown in the specification but is sequence (SEQ ID NO:2) shown in the
                                                                                                                                                                                                                                                                                                                                                          A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 generic sequence (AAE09181)
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Sequence

Matches Query Match

Local Similarity mes 42; Conserv

48.1%; ilarity 100.0%; Conservative

0;

Score 38; Pred. No. Mismatches

DB 22; hc. o. 2.4e-32;

Length 419; Indels

0;

Gaps

0;

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RESULT 15
AAE09213
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                                                                                                                         Misc-difference
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solid tumour; cancer; polymorphism; cytostatic; gene therapy;
p68HER-2; ECDIIIa; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE09213;
       Clinton G,
                       (UYOR-) UNIV OREGON HEALTH SCI.
                                       16-FEB-2000;
                                                       16-FEB-2001;
                                                                        23-AUG-2001
                                                                                        WO200161356-A1
                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human p68HER-2 generic protein variant 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE09213 standard; Protein; 419 AA.
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                                                     2001WO-US05327
                                       2000US-0506079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                            /note= "p68HER-2 c
substituted with I
e 356
                                                                                                                                                                            /label= Unknown
376
                                                                                                                                                                                                                                                                                                              /note= "Represented as
in the specification"
125
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                                                                                                         /note= "p68HER-2
substituted with
                                                                                                                                                                                                                                                                                               /note= "Represented as
in the specification"
                                                                                                                                                                                                                                                                                                                                                /label= ECDIIIa_variant
/note= "Extracellular d
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                                                                                                                                 label= Unknown
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       Evans A;
                                                                                                        generic sequence (AAE09181) Xaa
Asn"
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Leu*
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                                                                                                                                                                                                                                                                                                      the parent sequence shown
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                                                                                                                                                                                                                                                                                                                                shown
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Example 11; Page -; 61pp; English. New polypeptide, which binds to the the treatment of hard tumors -WPI; 2001-529934/58 extracellular domain of HER-2 for

The invention relates to novel HER-2 (herstatin-2) antagonist

containing a polypeptide that binds to the extracellular domain (ECD)

conf HER-2 at a site that is different from the binding site of humanised

antibody, Herceptin, at an affinity of at least 10°8. The present

invention is based upon the initial discovery of an alternative HER-2

many transcript with 274 bp insert of intron 8. The translation product

of the alternative transcript is a truncated HER-2 protein designated

possented by the contains ECD I, II of the pl85HER-2 and the novel ECDIIIa.

The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise

the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the

containing ECDIIIa versant sequence is human p68HER-2 generic protein

containing ECDIIIa variant sequence. Note: The present sequence is not shown in the specification but is derived from p68HER-2 generic sequence (SEQ ID NO:2) shown in the sequence listing (AAE09181).

Sequence 419 AA;

Duery Match
Best Local Similarity
watches 42; Conserve 밁 Š 347 7 PRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 388 PRPAAVPVPXRXQPXPAHPVLSFLRPSWDXVSAFYSLPLAPL 48 Conservative 48.18; 0; Score 38; Pred. No. Mismatches DB 22; 2.4e-32; Length 419 Indels 0; Gaps

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January 14, 2003, 17:10:35; Search time 14.3032 Seconds (without alignments) 1215.012 Million cell updates/sec
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419
1 MELAALCRWGLLLALLPPGA.....VGRGXDPDAHVAVXLSRYEG 419

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ć	2 C) (L	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	Մ1	4	ω	2	1	NO.	•	
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-1- SUBCELLULAR LOCATION: Type I membrane protein.	-1- SUBURIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS	-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate	ALTHOUGHT NEUKEGULINS DO NOT LITERACT WITH IT ALONE. GF30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-ALDHA AND AMPHREGULIN	-!- FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX,	dization.";	Ehsani A., Low J., Wallace R.B., Wu A.M.; "Characterization of a new allele of the human ERBB2 gene by allele-	MEDLINE=93194196; PubMed=8095488;	[4] [4] [7] [7] [7] [7] [7] [7] [7] [7] [7] [7	,	"A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal growth factor-receptor gene and is amplified in a	, Yamamoto T.;	SEQUENCE OF 737-1031 FROM N.A. MEDLINE=86016729; PubMed=2995967;	Science 230:1132-1139(1985). [3]	shares chromosomal location with neu oncogene.";	"Tyrosine kinase receptor with extensive homology to RGF receptor	McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,	MEDLINE-86070181; PubMed-2999974;	SEQUENCE FROM N.A.	Nature 319:230-234(1986).	"Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor receptor.":	Saito T., Toyoshima K.;	Comba V Nomina N Winstins	SEQUENCE FROM N.A.		<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</pre>	Homo sapiens (Human).		(p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell	(Rel. 41, Last annotation update)	13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last segmence undate)	P04626;	HUMAN	T = 1

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EMBL; M11764; AAA35;
EMBL; M11765; AAA358;
EMBL; M11766; AAA358;
EMBL; M11730; AAA7549;
MBL; M13363; CAA7706;
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RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654-ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654-ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654-VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
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PS001109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
brane; Glycoprotein; Multigene family; Receptor; Signal; ase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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; IPR001245; Tyr_pkinase.
; IPR004019; YLP_motif.
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MEDLINE-94193007; PubMed-7908275;

Nakamura T., Ushijima T., Ishizaka Y.,

Yamazaki Y., Ishikawa T.;

"Cloning and activation of the Syrian h
Gene 140:251-255(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precu.
(p185erbB2) (NEU proto-oncogene) (C-erbB-2)
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SUBUNIT: HETERODIMER
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15-JUN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
(p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth faceceptor-related protein).
ERBB2 OR NEU.
Rattice normalizations (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                       MEDILINE=92155181; PubMed=1346763;
Gullick W.J., Bottomley A.C., Lofts F.J., Doak D.G., Muln Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D. "Three dimensional structure of the transmembrane region oncogenic and oncogenic forms of the neu protein.";
EMBO J. 11:43-48(1992).
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Mammalia; Eutheria;
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SUBURIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECE
THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT FORMS
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYRC
                                                                                                                                                                                                                                                                                      FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GEPOTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY ECATALYTIC AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + pr tyrosine phosphate.
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een the Swiss Institute of Bioinformatics and the EN
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. Usage by a
                                                                                                                         http://www.isb-sib
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; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                   Mulvey
I.D.;
                                                                                                                                                                                                                                                                            RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor-related
                                                                                                                                                                                                                                       TYROSINE
                                                                                                                                                            restrictions
                                                                                                                                       and
                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                          GP30
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                                                                                                                                                                                                                                                              A HOMODIMER
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3P30 IS A
3GF, TGF-
                                                                                                                                                                          a collaboration -
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On
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RESULT 4
RNFE_VIBCH
ID RNFE_V
AC Q9KT91
DT 15-JUN
DT 15-JUN
DT 15-JUN
DT 15-JUN
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                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                             Matches
             RNFE_VIBCH
Q9KT91;
15-JUN-2002
15-JUN-2002
15-JUN-2002
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DISULFID
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NP_BIND
BINDING
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VARIANT
SEQUENCE
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Multigene family; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00261; FU; 3. SMART; SM00219; TyrKc; 1.
    Electron
                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000001; Euk_pkinase;
                                                                                                                  232
                                                                                                                                      231 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
                                                                                                                 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00069;
PF00757;
                                                                                                                                                                      Similarity
(Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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655
678
159
1723
728
755
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196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pkinase; 1.
furin-like;
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recep_L_domain;
                                                                                                                                                                                                       AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disease mutation
                                                                                                                                                                                                                                                                                                                                          1257
6544
12577
12577
12677
9846
9846
9846
1369
1369
1369
1369
1578
1578
1578
1578
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1141
1250
68
188
260
532
573
631
                                                                                                                                                                      12.2%;
                                                                                                                                                                                                        138831
                                                                                                                                                                      .0%;
                                                                                                                                                           Score 51; DB: Pred. No. 2.2 0; Mismatches
                                                                                                                                                            0
                                                                                                                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY
BY SIMILA
                                                                                                                                                                                                        WW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR PROTE EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase; ATP-binding;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
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                                                         230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN-TYROSINE ULAR (POTENTIAL).
                                                                                                                                                                      2 E
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                                                         8
                                                                                                                                                          .2e-43;
s 0;
                                                                                                                                                                                                                                                                                            (AUTO-)
                                                                                                                                                                                Length 1257;
                                                                                                                                                                                                      NEU).
CRC64;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                       -) (BY SIMILARITY).
-) (BY SIMILARITY).
) (POTENTIAL).
) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ptor; Signal;
Phosphorylation;
                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                 282
                                                                                                                                      281
                                                                                                                                                           0;
                                                                                                                                                           Gaps
                                                                                                                                                           0;
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                                                                                                                                                                               RESULT 5
EGFR_CHICK
    밁
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                  TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
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Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNFE OR
   SEQUENCE FROM N.A. MEDLINE=88261272;
                                                                                                                                                           P13387;
                                                         Archosauria;
                                                                    Eukaryota;
                                                                                                                                                                      EGFR_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                   NCBI_TaxID=9031;
                                                                                                    (Fragment).
                                                                                                                                                                                                                             184 LLALLPPGA 192
                                                                                                                                                                                                                                                  12 LLALLPPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR VC1012
                                                                                                                                                                                                                                                                                                                transport;

39

4 69

4 93 1

4 124 1

182 2

230 AA;
                                                                                                                                                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          IPR003667;
                                                                   Metazoa;
                                                         Aves;
                                                                                                                                                                                                                                                  20
    PubMed=3260329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-EI TOT N16961 / Serotype 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., Whité O.

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.

Fraser C.M.;
                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epidermal growth factor receptor precursor (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: May be part of a membrane complex transport (By similarity).
-I- SUBJUIT: Composed of at least six subunits; rnfD, rnfE and rnfG (By similarity).
-I- SUBCELLUIAR LOCATION: Integral membrane prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE004183; AAF94173.1; -. TIGR; VC1012; -.
                                         Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE NORDE/RNFAE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholerae.
ia; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rnf-Nqr;
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
59 POTENT
89 POTENT
113 POTENT
144 POTENT
202 POTENT
202 POTENT
202 POTENT
202 POTENT
Chordata; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rnf_Nqr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a
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                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 9;
Pred. No
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POTENTIAL.
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Craniata; Ver 
; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane complex involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Vibrionaceae;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                         703
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DB
Vertebrata; Eute
nes; Phasianidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 230;
                                                                                                   2.7.1.112)
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                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                 Euteleostomi;
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Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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DISULFID
CARBOHYD
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DOMAIN
DISULFID
DISULFID
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Pfam; PF00757; Furin-like; 1, PF100757; Furin-like; 1, PF101030; Recep_L_domain; 2.
SMART; SM00261; FU; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lax I.,
Ullrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
PROSITE; PS00109; PROTEIN_KINASE_TYR; PARTIAL.
PROSITE; PS50011; PROTEIN_KINASE_DOM; PARTIAL.
Transmembrane; Glycoprotein; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyrosine-protein
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P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. They by non-profit institutions as long a fitted and this statement is not removed ities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: Binding of EGF to the receptor leads to dimerization, internalization of the EGF-receptor complinduction of the tyrosine kinase activity, stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induction of the tyrosine kinase activity, stir
synthesis, and cell proliferation.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It een the Swiss Institute of Bioinfo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M20386; AAA48760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson
A., Venn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A., Vennstrom B., Schlessinger J., Glvol D.; epidermal growth factor (EGF) receptor: cDNA c on in mouse cells, and differential binding of ming growth factor alpha.";

1. Biol. 8:1970-1978(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000494;
IPR000719;
        kinase;
      EGFR_L_domain.
Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Phosphorylation.
COTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY

BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ght. It is produced
Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GROWTH FACTOR RECEPTOR.
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MEDLINE-84219729; PubMed-6528312;
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Lee J., Yarden Y., Libermann T.A., Schlessinger J., Down
Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
Miman epidermal growth factor receptor cDNA sequence an
expression of the amplified gene in A431 epidermoid carc
        MEDLINE=21100872; PubMed=11161793;
Reiter J.L., Threadgill D.W., Eley G.D., Str
Schehl Sinclair C., Pearsall R.S., Green P.J
Balasubramaniam S., Crossley T.D., Magnuson
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Mammalia; Eutheria;
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                                                                                                           Ilekis J.V., Gariti J., Niederberger 
"Expression of a truncated epidermal 
protein (TEGFR) in ovarian cancer."; 
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                                                                                                                                                                 MEDLINE=97256547;
                                                                                                                                                                                                                                                   Reiter J.L., Maihle N.J.;
"A 1.8 kb alternative transcript from
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Maihle N.J.;
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O'Malley B.W.
"Isolation of
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Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wi Roe B.A., Merlino G.T., Pastan I.;
"Human epidermal growth factor receptor cDNA is variety of RNAs overproduced in A431 carcinoma co Nature 309:806-810(1984).
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MEDLINE-89278137;
Margolis B.L., La.
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Biol. Chem. 266:1746-1753(1991).
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MEDLINE=88217333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin C.R., Chen W.S., Kruiger W., Stolarsky
Evans R.M., Verma I.M., Gill G.N., Rosenfo
"Expression cloning of human EGF receptor
amplification and three related messenger
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71:1-20(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96398132; PubMed=8962717;
Smith K.D., Davies M.J., Bailey D., Renouf D.V.,
Smith K.D., Davies M.J., Bailey D., Renouf D.V.,
"Analysis of the glycosylation patterns of the e
                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitogens.
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[17]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the epidermal growth ovary fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carpenter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20198209; PubMed=10731668;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U. Rev. Biochem. 56:881-914(1987).

FUNCTION: Receptor for EGF, but also for other members of the Enfamily, as TGF-alpha, amphiregulin, betacellulin, heparin-bindin EGF-like growth factor, GP30 and vaccinia virus growth factor. Involved in the control of cell growth and differentiation.

FUNCTION: Isoform 2/truncated isoform may act as an antagonist.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: Binding of EGF to the receptor lead dimerization, internalization of the EGF-receptor induction of the tyrosine kinase activity, stimula
                                                                                                                                                                                                                                                                                                             synthesis, and cell proliferation. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                    alternative splicing. TISSUE SPECIFICITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 4 isoforms; truncated isoform/TEGFR, 3/p110 ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein. Isoform
                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                expressed in ovarian cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted
                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It
sen the Swiss Institute of Bioinfi
European Bioinformatics Institute
X00588;
U95089;
U48722;
U48723;
U48724;
U48725;
U48726;
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                                                                                                                                                       non-profit institutions as long a land this statement is not removed. requires a license agreement (See lan email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G
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                  CAA25240.1;
AAB53063.1;
AAC50802.1;
AAC50804.1;
AAC50796.1;
AAC50797.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor
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Abe Y., Saito n.,
f the N-oligosaccharides
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                                                                                                                                                                                                                                      Bioinformatics an titute. There are
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in their carboxyl-terminal
EGF receptor.";
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) and 4; ar
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epidermal growth factor
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in Chinese hamster
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Q01279;
Q1-FEB-1996
Q1-FEB-1996
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[6]
                                                                                                                               Eisinger D.P., Serrero G.;
submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL-
AND ALSO OF TGF-KLPHA, AMPHIREGULIN, HEPARIN-BINDING EGF,
VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luetteke N.C., Phillips H.K.,
Jenkins N.A., Lee D.C.,
"The mouse waved-2 phenotype
receptor tyrosine kinase.";
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                                                                                                                                                                                                                                                                                                                                              binding site
                                                                                                                                                                                                                                                                                                                                                MEDLINE=91232866; PubMed=2030916;
Avivi A., Lax I., Ullrich A., Schlessinger
"Comparison of EGF receptor sequences as a
binding site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=B6/C3; TISSUE=Liver;
MEDLINE=94170986; PubMed=81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/c;
Hibbs M.L.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Avivi A., Skorecki K., Yayon A., Givol D.;
"Promoter region of the murine fibroblast growth factor receptor (bek/KGFR) gene.";
Oncogene 7:1957-1962(1992).
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
"Expression of the epidermal growth factor receptor
in mouse blastocysts during delayed implantation.";
Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
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tyrosine phosphate.

tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

MISCELLANBOUS: Binding of EGF to the receptor leads to

dimerization, internalization of the EGF-receptor complex,

income of the tyrosine kinase activity, stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCAAGCTGP
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9; Conser
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41,
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PubMed=7678348;
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Pfam; PF00757; Furin-like;
Pfam; PF01030; Recep_L_doma
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SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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U03425; AAA17899.1;

X59698; CAA42219.1;

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P11362; 1FGK.
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an email to license@isb-sib.ch).
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl
                                                                                                                                                                                                                                                                                                                   EMBL; X84349; CAA59088.1; -.
EMBL; X95986; CAA65230.1; -.
HSSP; P50162; IAE1.
InterPro; IPR002198; ADH_short.
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-!- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+)
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"Cloning and expression of carbonyl reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley; TISSUE=Tes
MEDLINE=95220378; PubMed=7705364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98295987; pubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holl-Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J. Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from tomplete genome sequence.";
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30-MAY-2000 (Rel. 39, Last sequence
15-JUN-2002 (Rel. 41, Last annotatic
Hypothetical protein Rv3130c.
RV3130C OR MT3216 OR MTCY03A2.28 OR
                                                          Hypothetical protein; Complete proteome.

CONFLICT 268 268 L -> F (IN REF. SEQUENCE 463 AA; 50720 MW; 48CC60A8670F1
                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE UPF0089 FAMILY.
                                                                                                                                   EMBL; Z95150; CAB08399
EMBL; AE007137; AAK475
TIGR; MT3216; -.
TubercuList; Rv3130c;
                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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NCBI_TaxID=1773;
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Barbas J.A., Chaix J.C., Steinmetz M., G.
"Differential splicing and alternative pc distinct NCAM transcripts and proteins in EMBO J. 7:625-632(1988).
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O1-JAN-1990 (Rel. 13,
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Neural cell adhesion m
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STRAIN-CS7BL/6;
MEDLINE-67246524; PubMed-3595563;
MEDLINE-67246524; PubMed-3595563;
MEDLINE-67246524; PubMed-3595563;
METHELS D., Santoni M.-J., Wille W., Ruppert C., Caix J., William C., Willia
                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6; TISSUE-Brain; MEDLINE-89251563; PubMed-2721486; MEDLINE-89251563; PubMed-2721486; Santoni M.J., Barthels D., Vopper G., "Differential exon usage involving an generates at least eight types of NCAN EMBO J. 8:385-392(1989).
                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural and immunological characterization of the a domain of mammalian neural cell adhesion molecules."; J. Biol. Chem. 261:3396 3401(1986).
                                                                                                                                                                                                                                                                                                                                                                                                              between
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NCAM1 OR NCAM
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NCA2_MOUSE
IL; Y00051; CAA68263.1;

IL; X15049; CAA33148.1; I

IL; X07195; CAA30173.1;

IL; X07195; CAA30173.1;

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MGI:97281; NCaml

D; MGI:97281; NCaml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEURITES, ETC.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-and ALTERNATIVE PRODUCTS: 3 isoforms; N-CAM 180 (AC P13595), N-(AC P13595) and N-CAM 120 (shown here); are produced by alternative splicing.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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molecule 1, 120 kDa isoform precursor (N-CAM 120)
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Pfam; PP00041; fn3; 2.
Pfam; PF00047; ig; 5.
SMART; SM00408; IG2; 5.
SMART; SM00408; IGC2; 5.
Cell adhesion; Glycoprotein; R
Immunoglobulin domain; Signal;
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O1-JAN-1990 (Rel. 13,
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Neural cell adhesion n
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MEDLINE=88059265; PubMed=3680385; Small S.J., Shull G.E., Santoni M.-J., Akeson "Identification of a cDNA clone that contains sequence for a 140-kD rat NCAM polypeptide."; J. Cell Biol. 105:2335-2345(1987).
                                                                           TISSUE=Brain;
                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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oa; Chordata;
ia; Rodentia;
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IG-LIKE C2-TYPE DOMAIN 3.
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HEPARIN-BINDING (POTENT
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REF. 2 AND 3).
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GPI-anchor
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; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90166485; PubMed=2483093; Small S.T. Hairry 7
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SEQUENCE OF
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SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I me ALTERNATIVE PRODUCTS: A number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THIS PROTEIN IS NEURON-NEURON ADHESION, NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; X06564; CAA29809.1; -.; M32611; AAA41679.1; -. S00846; IJRTNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                  VTAEDGTQ 329
VTAEDGTQ
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PF00047; ig; 5.
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SM00408; IGC2;
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8; Conser
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IPR003006; Ig_MHC.
IPR003598; Ig_c2.
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domain; Alter
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

IG-LIKE C2-TYPE DOMAIN 4.

IG-LIKE C2-TYPE DOMAIN 5.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.
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HEPARIN-BINDING
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N-LINKED (GLCNAC
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RESULT
NCA1_MO
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01-JAN-1990 (Rel. 1
01-JUL-1993 (Rel. 2
15-JUN-2002 (Rel. 4
                                                                                          J. Biol.
                                                                                                                                                                                   Santoni M.J., Barthels D., Vopper G., Boned A., "Differential exon usage involving an unusual sp generates at least eight types of NCAM cDNA in mEMBO J. 8:385-392(1989).
                                                                                                                                                                                                                      SEQUENCE OF 702-1115 FROM N.A. (I: STRAIN-C57BL/6; TISSUE-Brain; MEDLINE-89251563; PubMed-2721186; Santoni M.J., Barthels D., Vopper
                                                                                                                                                                                                                                                                                               "NCAM-180,
the mouse,
                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=88283628; PubMed=3396534;
Barbas J.A., Chaix J.C., Steinmetz M.,
"Differential splicing and alternative
distinct NCAM transcripts and proteins
EMBO J. 7:625-632(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse neural cell adhesion molecule (Na alternative RNA splicing.";
Nucleic Acids Res. 15:8621-8641(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Santoni M.-J., Barthels D., Be
Goridis C., Wille W.;
"Analysis of cDNA clones that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                  domain of mammalian neural
                                                                                                                                         Rougon G., Marshak D.R.;
                                                                                                                                                    MEDLINE-86140120;
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                                                                                                                                                                                                                                                                                     Nucleic
                                                                                                                                                                                                                                                                                                                      Barthels D., Vopper G., Wille
                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Brain; MEDLINE=88247737; PubMed=2454455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 529-1115 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and nucleotide sequence of mouse NCAM cDNA that a Mr 79,000 polypeptide without a membrane-spanning region. EMBO J. 6:907-914(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barthels D., Santoni M.J., Wille W., Hirsch M.R., Fontecilla Camps J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6;
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                                                                                                                               "Structural and
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splicing.
SIMILARITY:
SIMILARITY:
                                 SUBCELLULAR LOCATION: ALTERNATIVE PRODUCTS: 140 and N-CAM 120 (AC
                                                                                         Siol. Chem. 261:3396-3401(1986).
FUNCTION: THIS PROTEIN IS A CELL ADHESION
                                                                   NEURON-NEURON ADHESION, NEURITES, ETC.
                                                                                                                                                                                                                                                                                   se, is encoded by an alternatively Acids Res. 16:4217-4225(1988).
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BELONGS T
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                                                                                                               immunological characterization of the lian neural cell adhesion molecules.";
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41, Last annotation
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Rodentia;
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                                 P13594);
                                            Type I membrane page 3 isoforms; N-CAM
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           THE
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IMMUNOGLOBULIN-LIKE
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Sciurognathi;
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EMBL; Y00051; -; NOT_ANNOTATE!
EMBL; X06328; CAA29641.1; ---
EMBL; X07195; CAA30173.1; ---
EMBL; X07244; CAA30230.1; ---
EMBL; X15052; CAA33150.1; ---
EMBL; X15052; CAA33151.1; ---
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Pfam; PF00047; ig; 5.
SMART; SM00060; FN3; 2.
SMART; SM00408; IGC2; 5.
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Cell adhesion; Glycoprotein;
Immunoglobulin domain; Alterr
SIGNAL 1 19
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
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MGI:97281; NCam1.
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CAA29641.1; -.
CAA30173.1; -.
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: sequence up
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 4.

IG-LIKE C2-TYPE DOMAIN 5.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.
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ZOPORM N
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Homo sapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria; associated protein NGFRAP1 OR NADE.

Chordata; Primates;

Craniata; Ve Catarrhini;

Vertebrata;

Euteleostomi;

Hominidae;

Homo

(Human)

Mammalia; Eutheria; NCBI_TaxID=9606;

Rapp G., Freudenstein
Scheit K.H.;

J.,

Klaudiny J.,

Mucha

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Wempe F.,

MEDLINE=91025550; PubMed=2171551;

SEQUENCE FROM TISSUE-Ovary;

N.A.

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RESULT 14

NADE_HUMAN STAI Q00994; 01-JUN-1994 (Rel. 01-JUN-1994 (Rel. 15-JUN-2002 (Rel.

STANDARD;

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p75NTR-associated

29, Created)
29, Last sequence update)
41, Last annotation update)
cell death executor (Nerve on 1) (Ovarian granulosa cell

xecutor (Nerve growth factor receptor granulosa cell 13.0 kDa protein HGR7

HGR74).

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Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
use by non-profit institutions as long as its content is
modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
-!- FUNCTION: Involved in protein export (By similarity).
-!- SUBUNIT: Component of the protein translocase complex (By
                                                                                                                                                                        PROSITE; PS01067; SECE_SEC61G; FAI Protein transport; Translocation; TRANSMEM 40 60 POTEN
                                                                                                                                                                                                                          InterPro; IPR001901; SecE_euk_arch.
InterPro; IPR004795; SecE_euk_arch.
TIGRRAMS; TIGR00327; secE_euk_arch; 1.
PROSITE; PS01067; SECE_SEC61G; FALSE_NGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allar Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B De Woors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tol Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECE OR SSO5663
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE006668; AAK40677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
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SUBCELLULAR LOCATION: Tail-anchored membrane
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             Similarity 7; Conser
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             Score 7; DB Pred. No. 8.
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CD51874F424BE9FA CRC64;
                                                                                                                                                                                                      Transmembrane; Complete proteome
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                                                                      Length 62;
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15-DEC-1998 |
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30-MAY-2000 |
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Progonadoliberin II precursor [Contains: Gona
[Luteinizing hormone releasing hormone II] (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: May be a signaling adaptor molecule involved in p75NTR-mediated apoptosis induced by NGF. May play an important role in the pathogenesis of neurogenetic diseases.
---- SUBUNIT: Binds to the DEATH domain of p75NTR/NGFR.
---- TISSUE SPECIFICITY: FOUND IN OVARIAN GRANULOSA CELLS, TESTIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDITINE=20298829; PubMed=10764727;
Mukai J., Hachiya T., Shoji-Hoshino S., Kimura M.T., Nadano D.,
Mukai J., Hanaoka T., Li Y., Irie S., Greene L.A., Sato T.A.;
Suvanto P., Hanaoka T., Li Y., Irie S., Greene L.A., Sato T.A.;
"NADE, a p75MYR-associated cell death executor, is involved in signal
transduction mediated by the common neurotrophin receptor p75NTR.";
J. Biol. Chem. 275:17566-17570(2000).
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                        TISSUE=Hypothalamus;
MEDLINE=97079639; PubMed=8921350;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Tupaia glis
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                                                                  Fernald R.D.;
                                                                                            Kasten T.L., White S.A.,
                                                                                                                                                                                                                                                 NCBI_TaxID=9396;
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"Characterization of two new preproGnRH first direct evidence for mesencephalic
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L; BC003190; AAH03190.1;
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k; C35826; C35826.

Rew; HGNC:13388; NGFRAP1.
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                     Bond C.T., Adelman J.P.,
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Gen. Comp. Endocrinol. 104:7-19(1996).
-i- FUNCTION: STIMULATES THE SECRETION OF
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ALIGNMENTS

RESULT 1 A24571

protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming C;Speciles: Homo sapiens (man) C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999 C;Accession: A24571; A25491; A44188; B44188; I59509; I57622 R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; protein

N.; Miyajima, N.; Saito,

н

Nature 319, A; Reference number: A; Accession: A24571 A; Title: Similarity of protein encoded by the human c-erb-B-2 A; Reference number: A24571; MUID:86118663; PMID:3003577 230-234, 1986 gene to epidermal growt

A; Molecule type: mRNA A; Residues: 1-1255 < YAM>

A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198

-- R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985

A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid A;Reference number: A25491; MUID:86016729; PMID:2995967

A;Accession: A25491

A; Molecule type: DNA A; Residues: 737-1031 <SEM>

R;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; R;Coussens, L.; Yang-Feng, T.L.; Llao, Y.C.; Chen, E.; Gray,

PID:g553282 A.; McGrath, J.; Seeburg

R; Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, Science 230, 1132-1139, 1982.

A; Fitle: Tyrosine kinase receptor with extensive homology to Pa; Reference number: A44188; MUID:86070181; PMID:2999974

A; Accession: A44188 EGF receptor shares chro

A;Molecule type: DNA A;Residues: 740-910 <COU1> A;Cross references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A;Molecule type: mRNA
A;Residues: 1-517,'RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cross-references: GB:M11730; NID:g183986
A;Cross-references: GB:M11730; NID:g183986

-R;King, C.R.; Kraus, M.H.; Aaronson, -Science 229, 974-976, 1985

A;Title: Amplification of a A;Reference number: I59509; A;Accession: I59509 novel v-erbB-related gene in a human mammary carcinoma MUID:85272597; PMID:2992089

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 832-909 < REX>

A;Cross-references: GB:L29395; NID:g459807; IR;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, Mol. Cell. Biol. 7, 2597-2601, 1987 PIDN: AAA35809.1; PID:g459808 Α., Schlessinger, J.; Givol,

A;Reference number: I57622; MUID:87286898; PMID:3039351
A;Accession: I57622 Þ

A; Status: translated from GB/EMBL/DDBJ

A; Molecule type: DNA

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C;Super......
C;Keywords: ATP
C;Keywords: ATP
F;718-983/Domain: protein kinase
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F;22-1255/Product: protein-tyrosine kinase erbb2 #status predicted <MAT>
F;22-653/Domain: extracellular #status predicted <EXT>
F;70-304/Domain: EGF receptor extracellular domain repeat <EE1>
F;70-304/Domain: EGF receptor extracellular domain repeat <EE2>
F;595-605/Domain: transmembrane #status predicted <TMM>
F;676-1255/Domain: intracellular #status predicted <INT>
F;676-1255/Domain: protein kinase homology <KINN>
F;718-983/Domain: protein kinase homology <KINN
F;726-734/Region: protein kinase ATP-binding motif
F;68,124,187,259,530,571,639/Binding site: carbohydrate (Asn) (covalent) #status F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pred
F;758/Active site: Lys #status predicted
F;753/Active site: Lys #status predicted
    RESULT
TVRTNU
                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-19
C;Accession: I48161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1; 813/3
A;Introns: 25/1; 75/3; 147/1; 813/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M16792; NID:g183983; C;Comment: Amplification and overexpression
                                                                                       밁
                                                                                                                                                                                                                                                                                                                  A;Gene: neu
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1254 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: I48161;
A; Accession: I48161
A; Status: preliminary; trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 140, 251-255, 1994
A; Title: Cloning and activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: ERBB2; NGL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148161
                                                                                                                                                                    Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 83
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                                                                                       231
                                                                                                                            231 LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a, T.; Ush
251-255,
                                                                                     LPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFES
                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHSGICELHCPALVTYNTDTFES
                                                                                                                                                                       l Similarity
51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                              GB:D16295;
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                                                                                                                                                              12.2%; oc. 100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUID:94193007; PMID:790827
                                                                                                                                                                                                                                                                                                                                                                            NID:g493236;
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                                                                                                                                                                                                                                                                                                             factor receptor;
                                                                                                                                                                                                                                                 homology <KIN>
ATP-binding motif
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Pred. No.
                                                                                                                                                                                                           Score 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMID:7908275
                                                                                                                                                                                        DB 2;
3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Le
2.9e-74;
                                                                                                                                                                                                                                                                                                                                                                              PIDN:BAA03801.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:AAA58637.1; PID:g553332 of this erbB-related gene occurs
                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                  kinase
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                                                                                     281
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                                        Matches
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A; Accession: A24562
A; Molecule type: mRNA
A; Residues: 1-1260 < SBAR>
A; Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R; Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith
Carcinogenesis 12, 1975-1978, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RnfE-related protein VC1012 [imported] - Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #++++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (As
F;691/Binding site: phosphate (Thr) (covalent) #status
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: authors translated the codon GCA for residue 25 C; Genetics:
A; Gene: neu
C; Superfamily: epidermal growth factor receptor; protei C; Superfamily: epidermal growth factor receptor; glyc C; Keywords: ATP; autophosphorylation; duplication; glyc F; 1-19/Domain: signal sequence #status predicted <SIGS
F; 20-1260/Product: protein-tyrosine kinase neu #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Nolecule type: DNA
A; Residues: 637-663,'V',665-702
A; Residues: 637-663,'V',665-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Direct DNA sequencing of the rat neu oncogene 2-thiazolyl] formamide or N-methyl-N-nitrosourea. A; Reference number: A61204; MUID:92035293; PMID:1682063
                                                                                          A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                          R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112) neu precursor C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #tex
C;Accession: A2456; A61104
                                                                                                                                                                                A;Cross-references: GB:AE004183; GB:AE003852; NID:g9655473; PIDN:AAF94173.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-230 <HEI>
                                                                                                                                                                                                                                                                                                    A;Reference number: A82035;
A;Accession: B82252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A61204
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Bargmann, C.I.; Hung, M. Nature 319, 226-230, 1986
                                                                                                                                       A; Gene: VC1012
                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                               A; Title: DNA Sequence of
                                                                                                                                                                                                                                                                                                                                                                       Nature 406, 477-483, 2000
                       Query Match
Best Local
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Best Local
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Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                            both chromosomes of the cholera 35; MUID:20406833; PMID:10952301
                                                                                          hypothetical protein HI1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%;
                       2.1%;
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                       Score
Pred.
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No.
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No.
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DB
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3e-42;
                       72
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                                             Length 230;
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                                                                                                                                                                                                                                                                                                                                               pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                Gwinn, M.L.;
H.; Dragoi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281
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                                                                                                                                                                                                                                                                                                                                                                                                                  Dodson, R.
I.; Sellers
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Gaps

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RESULT 7
GQHUE
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A;Cross-references: GB:M37394
C;Superfamily: epidermal growth factor receptor; protein kinase
                                                                                                                 epidermal growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Homo sapiens (man) C;Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999 C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Petch, L.A.; Harris, J.; Raymond, V.W.; Blasband, A.; Lee, Mol. Cell. Biol. 10, 2973-2982, 1990
A;Title: A truncated, secreted form of the epidermal growth A;Reference number: A36325; MUID:90258888; PMID:2342466
A;Accession: A36325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epidermal growth factor receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Oct-1997
C;Accession: A36325
C;Accession: A36325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Accession: A42032
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A36325
           A; Reference number: A; Accession: A00641
                           A; Title: Human epidermal gro
A; Reference number: A00641;
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A; Residues: 1-644 <PET>
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A;Experimental source: liver
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A; Residues: 1-527 <FLI>
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                                                                            Nature 309, 418-425, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: sequence extracted from NCBI backbone (NCBIN:76892, NCBIP:76893)
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100.0%; Pr
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100.0%; Pr
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                              growth factor receptor cDNA sequence and aberrant expression of
41; MUID:84219729; PMID:6328312
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b; Pred. No. 1.4
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A;Title: ATP-stimulated interaction between epidermal growth A;Reference number: A38023; MUID:84191554; PMID:8325948 A;Contents: annotation; receptor activity A;Note: the EGF receptor (and other tyrosine kinases) can re;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang,
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A; Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-7, 798-799, 'TD', 802-811, 'R', 813-942 <XUY>
A; Experimental source: A431 human carcinoma cells, which have large numbers of EGF re R, Lin, C.R.; Chen, W.S.; Kruiger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, Science 224, 843-848, 1984
A; Title: Expression cloning of human EGF receptor complementary DNA: gene amplificati A; Reference number: A43615; MUID:84196372; PMID:6326261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; R;Haley, J.D.; Waterfield, M.D. J. Biol. Chem. 266, 1746-1753, 1991 A;Title: Contributory effects of de Novo transcription and pre A;Reference number: A38672; MUID:91107677; PMID:1988448 A;Accession: A38672
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A; Residues: 1-1210 < ULL>
A; Residues: 1-1210 < ULL>
A; Cross-references: EMBL: X00588; NID: g31113; PIDN: CAA25240.1; PID: g757924
A; Note: the authors translated the codon AAG for residue 540 as Asn
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Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A; Title: Characterization and sequence of the promoter region of the human
A; Reference number: A25772; MUID: 85270438; PMID: 2991899
A; Accession: A25772
                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 25-30,'S',32-51,454-467 <WBB>
R; Russo, M.W.; Lukas, T.J.; Cohen, S.; St.
J. Biol. Chem. 260, 5205-5208, 1985
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                                                                                                                                     J. Biol. Chem. 260, 5205-5208, 1985 A;Title: Identification of residues in the A;Reference number: A60143; MUID:85182650; A;Accession: A60143
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A; Residues: 1-29 <HAL>
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Nature 309, 270-273, 1984
                            R; Mroczkowski, B.; Mosig, G.;
                                                                A; Molecule type: protein
A; Residues: 740-744, 'X', 746-747 < RUS>
                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A05281
                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A05281; MUID:84172183;
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Science 224, 294-297, 1984
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A; Residues: 1028-1210 <SIM>
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A; Residues: 713-964 <LIN>
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A; Residues: 1-29 <HA2>
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A; Residues: 1-29 <ISH>
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                                Cohen,
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                                                                                                                                                                         nucleotide binding site PMID:2985580
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PMID:6325948

factor receptor and supe

can nick d hang, C.P.;

double-stranded Walton,

G.M.;

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C; Genetics:
A; Gene: GDB:EGFR
A; Gene: GDB:EGFR
A; Gene: GDB:EGFR
A; Cross-references: GDB:120610; OMIM:131550
A; Map position: 7p12.3-7p12.1
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: AffP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; phosphoprotein; protein; protein; protein deficted <MAT>
F; 25-1210/Product: EGF receptor **status predicted <MAT>
F; 25-1210/Product: EGF receptor extracellular domain repeat <EE1>
F; 390-600/Domain: EGF receptor extracellular domain repeat <EE2>
F; 46-668/Domain: transmembrane **status predicted <TMM>
F; 669-1210/Domain: intracellular **status predicted <TMM>
F; 710-975/Domain: protein kinase homology <KIN>
F; 710-975/Domain: protein kinase homology <KIN>
F; 710-726/Region: coated-pit mediated internalization signal
- 10-1210/Region: inhibitory
- 10-1210/Region: inhibitory
- 10-1210/Region: inhibitory
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009
A; Residues: 689-694,'X',998-992,'XX',995-996,'X',998-1000;1002-1009
A; Residues: 689-694,'X',998-992,'XX',998-996,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-998,'X',998-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, Oncogene 6, 673-676, 1991

A; Title: Comparison of EGF receptor sequences as a guide to A; Reference number: A43818; MUID:91232866; PMID:2030916
A; Accession: A43818
A; Molecule type: mRNA
A; Residues: 1-714 <AVI>A; Residues: 1-714 <AVI>A; Cross-references: GB:X59698
B; Cross-references: GB:X59698
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                                                                                                                                                                                                                                                                                                           R;Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A;Title: Epidermal growth factor receptor threonine and serine
A;Reference number: A28941; MUID:88330814; PMID:3138233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: $24942
A; Accession: $24942
A; Molecule type: mRNA
A; Residues: 969-971, 'K', 973-1115, 'D'
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C;SpecLes: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: A53183; A43818; S24942; A28941; S45325; I49643
R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins,
                                                                                                                                                                                                                                                                      A; Accession: A28941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: U03425
R; Avivi, A.; Lax, I.; Ullrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The mouse waved-2 phenotype results from a point mutation A;Reference number: A53183; MUID:94170986; PMID:8125255 A;Accession: A53183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1210 <LU
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Pred. No.
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C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; phospho F;1-24/Domain: signal sequence #status predicted <SIG>F;1-64-GO/Domain: transmembrane #status predicted <TMM>F;712-977/Domain: protein kinase homology <KIN>F;720-728/Region: protein kinase ATP-binding motif F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental F;993/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental F;1028/Binding site: phosphate (Ser) (covalent) #status experimental F;1028/Binding site: phosphate (Tyr) (covalent) #status experimental
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A; Residues: 1-971, Kr., 973-1210 < VER>
A; Residues: 1-971, Kr., 973-1210 < VER>
A; Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55587.1;
A; Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
A; Title: Expression of the epidermal growth factor receptor gen
A; Reference number: 149643; MUID:93126380; PMID:7678348
A; Accession: 149643
                                                                                                                                                                                                                                                                                                                                                                                                     R:Nilsen, T.W.; Maroney, P.A
Cell 41, 719-726, 1985
A;Title: C-erbB activation i
A;Reference number: A00643;
A;Accession: A00643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB C;Species: Gallus gallus (chicken) C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change C;Accession: A27720; A00643
F;31-654/Domain: extracellular #status predicted <EXT>
F;81-307/Domain: EGF receptor extracellular domain repeat <EE1>
F;837-610/Domain: EGF receptor extracellular domain repeat <EE2>
F;655-677/Domain: transmembrane #status predicted <TMM>
                                                                                                                     pecific protein kinase
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-1223/Product: epidermal growth factor receptor #s
                                                                                                                                                                                               A;Gene: erbB
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein
                                                                                                                                                                                                                                                                                                C; Genetics
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A; Residues: 585-1223 <NIL>
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A; Residues: 1-1223 <LAX>
A; Cross-references: GB: M20386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Chicken epidermal growth factor (EGF) receptor: A; Reference number: A27720; MUID:88261272; PMID:3260329
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A; Residues: 12-20, 22-132 <RES>
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A; Accession: S45325
A; Status: prelimina
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                                                                                                                  1223/Product: epidermal growth factor
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ein-tyrosine kinase (EC 2.7.1.112) erbB
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conserved hypothetical protein PA2771 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83298
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-140,'GM',143,'R',145-235,'T',237-238,'E',240-277 <
A;Cross-references: DDBJ:D89069; NID:91906811; PIDN:BAA19007.1;
A;Cross-references: DCBJ:D89069; NID:91906811; PIDN:BAA19007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X84349; NID:g666086; PIDN:CAA59088.1; R;TOft, E.; Soederstroem, M.; Ahlberg, M.B.; DePierre, J.W. Biochem. Biophys. Res. Commun. 201, 149-154, 1994
A;Title: A novel 34kDa glutathione-binding protein in mature ra A;Reference number: PC2159; MUID:94256971; PMID:8198567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carbonyl reductase (NADPH2) (EC 1.1.1.184), inducible - rat C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Apr-1997 #sequence_revision 18-Jul-1997 #text_change 03-Jun-2002 C;Accession: S68982; PC2234; JC5284; PC2159; S52349
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F;727-735/Region: protein kinase ATP-binding motif
F;127-735/Region: protein kinase ATP-binding motif
F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;192,650/Binding site: carbohydrate (Ser) (covalent) (by protein kinase C) #status predicted
F;687/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #state;754/Active site: Lys #status predicted
F;7100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #state
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A;Title: Identification of two closely related genes, induci A;Reference number: JC5284; MUID:97167735; PMID:9015353
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A; Residues: 104-121,'x',123-134,'D',136-137,'H'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Cloning and expression of carbonyl reductase from A; Reference number: S68982; MUID:95220378; PMID:7705364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Wermuth, B.; Maeder-Heinemann,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession:
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A;Residues: 1-277 <WER>
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Best Local
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Conservative 0;
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b; Pred. No. 8.2
0; Mismatches
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l; PID:g1906812
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M.J.; Bd
K.; Lim,
                                                                                                                            PAO1)
                                                                    A; Molecule type: mRNA
A; Residues: 1-725 < BARS,
A; Cross-references: EMBL: Y00051; NID: g53342; PIDN: CAA68263.1;
R; BarDas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation A;Reference number: S00382; MUID:88283628; PMID:3396534 A;Accession: S00382
                                                                                                                                                                                                 A; Title: Isolation and nucleotide sequence A; Reference number: A29673; MUID:87246524; A; Accession: A29673
                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision
C;Accession: A29673; S00382; A44290
                                                                                                                                                                                                                                                                           R; Barthels, D.; Santoni, EMBO J. 6, 907-914, 1987
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Santoni, M.J.; Wille, W.;

Ruppert,

С.;

Chaix,

J.C.; Hirsch, M.R.;

Fon

of mouse NCAM PMID:3595563

CDNA

that

codes for a

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PID:953343

generates distinct

precursor, GPI-anchored splice form -

31-Mar-1993

#text_change

31-Dec-2000

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.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome s
A; Reference number: A82950
A; Accession: B83298
                                                                                                                                               C;Geneti
A;Gene:
                                                                                                                                                                                     A;Cross-references: GB:Z95150; GB:AL123456; NID:g3250708; PIDN:CAB08399.1; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-463 <C
                                                                                                                                                                                                                                                                               A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: H70922
                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
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A; Residues: 1-341 <STO>
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Nature 393, 537-544,
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C;Accession: H70922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Rv3130c – Mycobacterium tuberculosis (strain H37RV)
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Best Local :
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                                   95 PLQRLRIV
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8; Conserv
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50; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                            Devlin, K.; Feltwell, T.; Gentles, S.; Ha
J.; Rutter, S.; Seeger, K.; Skelton, S.;
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Pred. No.
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A; Accession: A44290
A; Molecule type: protein
A; Residues: 20-36 <ROU>
C; Comment: KCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol.
C; Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
C; Genetics:
A; Map position:
C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C; Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
F; 1-19/Domain: immunoglobulin homology <IMM1>
F; 132-19/Domain: signal sequence #status predicted <SIG>
F; 152-156/Region: heparin binding #status predicted
F; 21-156/Region: heparin binding #status predicted
F; 228-290/Domain: immunoglobulin homology <IMM3>
F; 63-272/Region: NCAM binding #status predicted
F; 228-290/Domain: immunoglobulin homology <IMM4>
F; 420-482/Domain: immunoglobulin homology <IMM3>
F; 420-482/Domain: immunoglobulin homology <IMM4>
F; 420-482/Domain: immunoglobulin homology <IMM5>
F; 420-482/Domain: immunoglobulin homology <IMM
                                                                                                                                                                                                      A; Nolecule type: mRNA
A; Residues: 340-381 <SM2>
A; Residues: 340-381 <SM2>
R; Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A; Title: Polypeptide variation in an N-CAM
A; Title: Polypeptide variation in an N-CAM
A; Title: Polypeptide variation in an N-CAM
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J. Cell I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30
C;Accession: S00846; B37795; I58136
C;Accession: S00846; B37795; B8136
                                                A; Molecule type: DNA
A; Residues: 355-364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B37795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Expression of the unique NCAM VASE exon A; Reference number: A37795; MUID:91035620; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S00846
A; Molecule type: mRNA
A; Residues: 1-858 <SMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural cell adhesion molecule short domain form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: X06564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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    A;Cross-references:
                                                                                                                                                                                  A; Accession: I58136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Rougon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;519-596/Domain: fibronectin type III repeat homology <FN3A>;625-685/Domain: fibronectin type III repeat homology <FN3B>;41-96,139-189,235-288,330-386,427-480/Disulfile bonds: #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA; Residues: 642-656,'D',658-725; Residues: EMBL:X07195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;222,316,348,424,450,479/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Small, S.J.; Akeson, R.
Cell Biol. 111, 2089-2096, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rougon, G.; Marshak, D. Biol. Chem. 261, 3396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 VTAEDGTQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                  preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTAEDGTQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            names: NCAM-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S00846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
    GB:M32611;
                                                <RES>
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    NID:g205643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ision 30-Sep-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbohydrate
                                                                                                                                                                                                                                   extracellular immunoglobulin-like fold PMID:2483093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E exon is independently PMID:1699951
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    PIDN: AAA41679.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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PID:g205644
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lent) #stat
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A; Gene: NCAM
C; Superfamily
C; Keywords: a
F; 1-19/Domain
                                                                                                                                                                                                                                                                                                     A; Access type: mRNA
A; Molecule type: mRNA
A; Residues: 529-809,1077-1115 <SAN>
A; Cross-references: EMBL: X06328; NID: g53322; PIDN: CAA29641.1;
A; Cross-references: Chaix, J.C.; Steinmetz, M.; Goridis, C.
                                                        A;Reference number: A28281; MUID:88247737; PMID:245
                                                                                                               R; Barthels, D.; Vopper, G.; Wille, W. Nucleic Acids Res. 16, 4217-4225, 198 A; Title: NCAM-180, the large isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinr Nucleic Acids Res. 15, 8621-8641, 1987 A;Title: Analysis of cDNA clones that code for the transmembrane A;Reference number: S00844; MUID:88067687; PMID:3684567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-548,'T',550-571,'T',573-574,'D',576-588,'MQPS',593,'S',595-599,'P',601,
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
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                                                                                                                                                                                                                                                                        A; Title: Differential splicing and alternative polyadenylation A; Reference number: S00382; MUID:88283628; PMID:3396534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: A29673
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A: Title: Text-1
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F;161-165/Region:
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                       A; Residues:
                                               A;Molecule type:
                                                                                                                                                                                 A;Cross-references: EMBL:X07195
                                                                                                                                                                                                        A;Residues: 642-1115 <BAR>
                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                   A; Accession: S00384
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S00844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000:Accession: A29673; S00844; S00384; A28281; A44290; S00383; Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                722-739/Domain: transmembrane #status predicted <TMM>
740-858/Domain: intracellular #status predicted <INT>
41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-721/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 VTAEDGTQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Domain: signal sequence #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTAEDGTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adhesion molecule 1 precursor, long domain splice
                       804-1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conserv
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ternative splicing; brain; cell adhesion; duplication; heparin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neural cell adhesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin homology <IMM4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and nucleotide sequence of mouse NCAM A29673; MUID:87246524; PMID:3595563
EMBL:X07244;
                          <BA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adhesion molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.9%;
NID:g53321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                    1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score Fred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       short
                                                                                       PMID: 2454455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
PIDN:CAA30230.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             short
                                                                                                                 cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                               adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA
PID:g929720
                                                                                                                                                                                                                                                                                                                                                                PID:g817984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.C.; Hirsch, M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that codes for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               form -
                                                                                                                                                                                                                                                                                              generates
                                                                                                               molecule
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F;132-191/Domain: immunoglobulin homology <IMM2>
F;132-195/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;262-290/Domain: immunoglobulin homology <IMM4>
F;262-272/Region: NCAM binding #status predicted
F;262-388/Domain: immunoglobulin homology <IMM4>
F;262-388/Domain: immunoglobulin homology <IMM5>
F;419-596/Domain: fibronectin type III repeat homology <FN3A>
F;519-596/Domain: fibronectin type III repeat homology <FN3B>
F;712-789/Domain: fitransmembrane #status predicted <INM>
F;712-790/Domain: intracellular #status predicted <INM>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;262,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si F;1-19/Domain: signal sequence #status predicted <SIG>
F;10-1115/Product: neural cell adhesion molecule, long domain splice form #status experif;20-711/Domain: extracellular #status predicted <EXT>
F;30-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobalin homology <IMM1>
Search completed: January 14, 2003, 17:15:20 Job time: 45.3996 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: NCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of A;Reference number: A44290; MUID:86140120; PMID:3512556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۱; Residues:
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Best Local S
Matches 8
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                                                                                                                                                                                                         322 VTAEDGTQ 329
                                                                                                                                    98 VTAEDGTQ 105
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type: protein
20-36 <ROU>
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                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                      1.9%; Score 8; DB 100.0%; Pred. No. 28; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                          Length 1115;
                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                         0;
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